

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number

TO: Nita M Minnifield

Location: REM/3C01/3C18

Art Unit: 1645

Saturday, September 17, 2005

Case Serial Number: 10/002784

From: Edward Hart

**Location: Biotech-Chem Library** 

**REM-1A55** 

Phone: 571-272-2512

edward.hart@uspto.gov

#### Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 

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From:

Minnifield, Nita

Sent: To: Thursday, September 15, 2005 4:51 PM

To: Subject: STIC-Biotech/ChemLib sequence search

10/002784

#### STIC

Please do a commercial and interference sequence search on SEQ ID NO:16 and 27 of this application.

Please provide a paper copy of all results.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

RECEIVED

SEP 15 2005

STECH/CHEM. DIVISION

Type of Search
NA#\_\_\_\_\_AA#:\_\_\_\_
S/L:\_\_\_\_Oligomer:\_\_\_\_
Encode/Transl:\_\_\_\_
Structure #:\_\_\_\_Text:\_\_\_
Inventor:\_\_\_\_ Litigation:\_\_\_

Vendors and cost where applicable
STN:
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Search completed: September 17, 2005, 01:13:37
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                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
enterotoxin B at 1.5-A resolution: implications for superantigen recognition by MHC class II molecules and T-cell receptors."; J. MOL. Biol. 277:61-79(1998).

-!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases
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DQFLYFDLI -> NEFFDLIYL (in Ref. 3).
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InterPro; IPR006137; Bact Ladotox.
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InterPro; IPR006173; Stap/Strept tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PF01123; Stap_Strp_Cox C; 1.
Pfam; PF01123; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRITOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_1; 1.
BROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
3D_structure; Direct protein sequencing; Enterotoxin; Signal;
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PDB; 1D5X; X-ray; C=28-266.
PDB; 1D5X; X-ray; C=28-266.
PDB; 1D6X; X-ray; C=28-266.
PDB; 1SBB; X-ray; B/D=28-266.
PDB; 1SBB; X-ray; 0=28-266.
PDB; 1SBB; X-ray; 0=28-266.
PDB; 1SBB; X-ray; 0=28-266.
PDB; 2SBB; X-ray; D/H=29-262.
PDB; 3SBB; X-ray; D=28-266.
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gene in Escherichia
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enterotoxin B,
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MEDLINE-93063291; PubMed=1436058; DOI=10.1038/359801a0;
Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
CTystal structure of staphylococcal enterotoxin B, a superantigen.";
Nature 359:801-806(1992).
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Jardetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
Chi Y.I., Stauffacher C., Strominger J.L., Wiley D.C.;
"Three-dimensional structure of a human class II histocompatibility
molecule complexed with superantigen.";
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Jones C.L., Khan S.A.;
"Nucleotide sequence of the enterotoxin B gene from Staphylococcus
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MEDLINE-98181012; Pubmed=9514739; DOI=10.1006/jmbi.1997.1577;
Papageorgiou A.C., Tranter H.S., Acharya K.R.;
"Crystal structure of microbial superantigen staphylococcal
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Huang I.-Y., Bergdoll M.S.;
"The primary structure of staphylococcal enterotoxin B.
cyanogen bromide peptides of reduced and aminoethylated
and the complete amino acid sequence.";
J. Biol. Chem. 245:3518-3525(1970).
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MEDLINE-65298255; PubMed-3898073;
Manelli D.M., Jones C.L., Johns M.B., Mussey G.J.,
"Molecular cloning of staphylococcal enterotoxin B
coli and Staphylococcus aureus.";
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Bacteria, Firmicutes, Bacillales, Staphylococcus
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MEDLINE-99137798; PubMed=9952369;
Medlingahead S.K., Beall B.;
The "Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptoxocci.";
The "Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptoxocci.";
The "Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptoxoci.";
MEDL; AF029051; AAD21315.1;
MESSP; PO1552; 1SEB.
RO; GO:0005405; P:pathogenesis; IEA.
MESSP; PO1552; Bact modcox.
MITGEPTO; IPR0066123; Bact modcox.
MITGEPTO; IPR0066123; Stap/Strept.tox.
MITGEPTO; IPR0066123; Stap/Strept.tox.
MITGEPTO; IPR0066123; Stap/Strept.tox.
MITGEPTO; IPR0066123; Stap/Strept.tox.
MITGEPTO; PR006173; Stap. Strp. Lox.
MEDLICATION OF STAP. STRP. Lox.

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Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
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25884 MW; 121F8460992818F8 CRC64;
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receptor

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Streptococcus equisimilis.
                                                                                                                                                                                                                        Best Local Similarity 88.2*
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus.
NCBI_TaxID=119602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=speA;
                                                                                                                                                                         NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                  203
                                                                                                                          Signal.
NON TER
SIGNAL
                                                                                                                                                                                                              Query Match
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                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                       62 BLKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                         23 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT 82
                 speA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 VSIDGIQSLSFDIETNKKANTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
                                                                                                                                                                                                                                                                                                                                                           2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the speA
                                                                                                                                                                                                                                                                                                                                     Gaps
A Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

"Characterization and clonal distribution of four alleles of the greencoding pyrogenic exotoxin A (scarlet fever toxin) in Strepencoccus pyrogenic exotoxin A (scarlet fever toxin) in Strepencoccus pyrogenic exotoxin A (scarlet fever toxin) in Strepencoccus pyrogenic exotoxin A (scarlet fever toxin) in Go. Go. 144:1271-1274(1991).

B. Exp. Med. 174:1271-1274(1991).

R. GO, GO: 0005405; C: extracellular; IEA.

GO; GO: 0005405; C: extracellular; IEA.

GO; GO: 0005405; P: pathogenesis; IEA.

InterPro; IPR006123; Stap/Strep_toxin.

R. InterPro; IPR006123; Stap/Strep_toxin.

R. InterPro; IPR006123; Stap/Atrept tox.

R. InterPro; IPR006123; Stap/Atrept Lox.

R. Pfam; PF01123; Stap_Lox C; 1.

R. Pfam; PF02376; Stap_Lox C; 1.

R. PRINTS; PR00277; STAPH_STREP_TOXIN_1; 1.

R. PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                             2; Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
"Characterization and clonal distribution of four alleles of gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";
J. Exp. Med. 174:1271-1274(1991).
EMBL; X61573; CAA43771.1;
PIN; 181879; S18789.
HSSP; PO1552; 1SEB.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                           41.1%; Score 1027.5; DB 2; Length
98.0%; Pred. No. 1.4e-58;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmīcutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                     1 1 Potential.
23 >220 type A exotoxin.
220 220 WW; 92DB096E57906DF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Type A exotoxin precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MGAS156;
MEDLINE=92044323; PubMed=1940804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 SFWFDFFPEPEFTQSKYL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 SFWFDFFPEPEFTQSKYL 198
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.0
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus.
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=speA;
                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
                                                                                                                                                                                                                        Signal.
NON TER
SIGNAL
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Q54696
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ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 VSIDGIQSLSFDIETSKKMVTAQELDYKVRKHLTDNKQLYTNGPSKYETGYIKFISKDKE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 QQDPNPSQLHRSSLVKNLQNIYFLYEGDPVVHENVKSVDQLLSHDLIYNVSGLNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                              2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                            39.5%; Score 986.5; DB 2; Length 236; 88.2%; Pred. No. 6.9e-56; ive 13; Mismatches 11; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                        1 1 2 Potential.
23 >236 type A exotoxin.
236 236 236 3054120B79127DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008992; Bact_endotox.
InterPro; IPR00617; BactT_tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Stap/Strept_tox.
InterPro; IPR006128; Staph/Strept_tox.
InterPro; IPR006139; Stap, toxin; IPEam; PF01123; Stap, Errp_toxin; IPEam; PF02876; Stap_Strp_toxin; IPR01175; PR00279; BACTRLTOXIN.
PROSITE; PS00279; BACTRLTOXIN.
PROSITE; PS002778; STAPH_STREP_TOXIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 AA
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PRT;
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STRAIN-MGAS500;
MEDLINE-92044323; PubMed=1940804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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NON TER
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q79AQ0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VSIDGIQSLSFDIETINKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 VSIDGIQSLSFDIETNKKAMYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
                                                                                                                                                          speA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
               SEQUENCE FROM N.A.

STRAIN=MARS165, MGAS127, MGAS493, MGAS494, MGAS167, and MGAS156;

MEDINE=SQA04323; PubMed=1940804;

Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

"Characterization and clonal distribution of four alleles of the specace of the specace progenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";

L J. Exp. Med. 174:1271-1274(1991).

R EMBL; X61556; CAA43753.1; -..

R EMBL; X61559; CAA43756.1; -..

R EMBL; X61559; CAA43756.1; -..

R EMBL; X61559; CAA43756.1; -..

R EMBL; X61569; CAA43756.1; -..

R EMBL; X61569; CAA43756.1; -..

R EMBL; X61569; CAA43758.1; -..
                                                                                                                                                       the
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STRAIN=MGAS156, MGAS250, MGAS285, MGAS480, MGAS492, and
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43.8%; Score 1095.5; DB 2; Length 236;
Best Local Similarity 98.1%; Pred. No. 6.4e-63;
Matches 207; Conservative 1; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27454 MW; 3FB3F41ABDC13A84 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Type A exttoxin precursor (Fragment).
Name=speA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
type A exotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006126; Staph/Strept tox.
Pfam; PF01123; Stap_Strp_tox OB.
Pfam; PF01123; Stap_Strp_tox OB.
Pfam; PF02876; Stap_Strp_tox C; I.
PRINTS; PR00279; BACTRITOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN 1; I.
PROSITE; PS00278; STAPH_STREP_TOXIN 1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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22
>236
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<1
23 >2
236 2
236 AA;
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NCBI_TaxID=1314;
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NON TER
SEQUENCE
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SIGNAL
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ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 VSIDGIQSLSFDIETNKKWYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
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                                                                                                                           the
MEDLINE=92044323; PubMed=1940804;
MeDLINE=92044323; PubMed=1940804;
Melson K., Schlievert P.M., Selander R.K., Musser J.M.;
Melson Progenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";
Melson Med. 174.1271-1274(1991).
Melson K. Schisch (ZAA43760.1; -...)
Melson K. Schisch (ZAA43760.1; -...)
Melson K. Schisch (ZAA43762.1; -...)
Melson K. Melson K. Schip (ZAA-GAR)
Melson K. M
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Pred. No. 1.6e-62;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1 22 Potential.
23 >236 type A exotoxin.
236 AA; 27484 MW; 2EF7F41AACB53600 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Type A exotoxin precursor (Fragment).
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PRELIMINARY;

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SO THE PRESENTATION OF THE PRESENT O
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STRAIN=MGAS485, MGAS491, MGAS495, and MGAS624;

MEDLINE=92044323; PubMed=1940804;

A MEDLINE=92044323; PubMed=1940804;

A Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

"Characterization and clonal distribution of four alleles of the speat gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes ";

J. Exp. Med. 174:1271-1274(1991).

Exp. Med. 174:1271-1274(1991).

ExmBL; X61569; CAA43767.1;

ExmBL; X61569; CAA43766.1;

REMBL; X61570; CAA43768.1;

REMBL; X61571; CAA43769.1;

REMBL; X61571; CAA43776.1;

REMBL; X61088; A60108.

REMBL; K61089; A60108.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT 82
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43.9%; Score 1096.5; DB 2; Length
Best Local Similarity 98.6%; Pred. No. 5.5e-63;
Matches 208; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strepticoccus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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>236 type A exotoxin.
236
; 27468 MW; 29DF2AD575623A84 CRC64;
                                                                                                                                                                                                                054779; Q54613; Q54736; Q54740; Q54741; Q54779; Q54779; Q54771; Q547741; Q5
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GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph/Strept_tox.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_toxin; 1.
PRINTS; PR00277; STAPH_STREP_TOXIN 1; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Type A exotoxin precursor (Fragment)
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<1
23 >2
236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus.
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=speA;
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SEQUENCE
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SIGNAL
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                                                                               RESULT 7
Q54779
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RESULT 8 Q9R931

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121 VSIDGIQSLSFDIETNKKANTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A MALDINE-913/1917/1917 Pubmeds 9923409;

A Hollingshead S.K., Beall B.; Hollingshead S.K., Beall S.K., Britangshead S.K., Britangshead S.K., Britangshead S.K., Beall S.K., Britangshead S.K., Britangshead S.K., Back Endotox.

A GO, GO.0005405; Pipathogenesis; IEA.

B HSSP; PO1552; 1SEB.

GO, GO.0005405; Pipathogenesis; IEA.

B HASP; PO1552; Back Endotox.

B HASP; PO1552; Back Endotox.

B HASP; PO1552; Back Endotox.

B HASP; PO1553; Staph/Strept toxin.

B HASP; PO153; Staph/Strept tox.

B Fam; PPO153; Staph/Strept tox.

B Fam; PPO153; Staph/Strept tox.

B PROSITE; PS00279; STAPH STREP TOXIN. 1; 1.

B ROSITE; PS00279; STAPH STREP TOXIN. 2; 1.

B HOW TER.

B HO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
43.8%; Score 1095.5; DB 2; Length
Best Local Similarity 98.1%; Pred. No. 5.9e-63;
Matches 207; Conservative 1; Mismatches 2; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                           Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;
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P97163; P97164;

PAX-1997 (TERBLEL 03, Created)

01-MAY-1997 (TERBLEL 03, Last sequence update)

05-JUL-2004 (TERBLEL 27, Last annotation update)
                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFWFDFFPEPETQSKYLMIYKDNETLDSNT 211
                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=D709;
MEDLINE=99137798; PubMed=9952369;
                               01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
Exotoxin A (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus.
NCBI_TaxID=1314;
Q9R931;
01-MAY-2000 (
01-MAY-2000 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=speA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
P97163
ID P971163
AC P9711
AC P9711
DT 01-M
DT 05-J
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CS STREE
CC BECK
OC BECK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic
                                                                        -1- MISCELLANEOUS: This toxin seems to be coded by bacteriophage T12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Binds to major histocompatibility complex class II beta
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=86166804; PubMed=3514452;
Weeks C.R., Ferretti J.J.;
"Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
Papageorgiou A.C., Collins C.M., Guman D.M., Kline J.B.,
O'Brien S.M., Tranter H.S., Acharya K.R.;
"Structural basis for the recognition of superantigen streptococcal pyrogenic exotoxin A (SpeAl) by MHC class II molecules and T-cell EMBO J. 18:9-21(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=86284313; PubMed=3526093;
Johnson L.P., L'Italien J.J., Schlievert P.M.;
Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus enterotoxin B.";
Mol. Gen. Genet. 203:354-356(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                  Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006177; BctrI_tox.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF02876; Stap_Strp_tox_C; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bctr1_tox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun. 52:144-150(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus.
NCBI_TaxID=1314;
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ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 VSIDGIQSLSFDIETNKKMYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 QQDPDFSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQDPDPSQLHRSSLVKNLQNI YFLYEGDPVTHENVKSVDQLRSHDLI YNVSGPNYDKLKT
                                                                                                                                                                  I -> L (in Ref. 2).
TNKKMVTAQELDYK -> QIKNGNCSRISYT (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                              ?
                                                                                                  VT -> MK (in Ref. 2).
SQEVFAQQDPD -> LPKGICSTRPK (in Ref. 4).
H -> Q (in Ref. 2).
S -> N (in Ref. 2).
NLQNIYFLYEGDP -> TFKIYIFFMRVTL (in R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29246 MW; 54001FE4CCCBFCC3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.2%; Score 1129; DB 1; 97.7%; Pred. No. 4.7e-65;
                                                                   Exotoxin type A.
                                                                                          -> E (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.7e
1; Mismatches
Pfam; PF01123; Stap_Strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH STREP_TOXIN_2; 1.
3D-structure; Signal; Toxin.
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Matches 216; Conservative
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251
128
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                                                         SIGNAL
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Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
    25-OCT-2004 (Rel. 45, Last annotation update)
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Matches 216; Conservative
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                   Streptococcus
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SEQUENCE
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    DDI BERNAMAN BERNAMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=SSI-1;
MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.,
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                 STRAIN=MGAS315 / Serotype M3;
MEDLINE=2213808; PubMed=12122206; DOI=10.1073/pnas.152298499;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Parkins L.D.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00279; BĀČTRLTOXIN.
PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
PROSITE; PS00278; STAPH STREP_TOXIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A60108; A60108.
HSSP, P01552; 1SEB.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006173; Stapl/Strept toxin.
InterPro; IPR006126; Staph/Strept toxin.
InterPro; IPR006126; Staph/Strept toxin.
InterPro; IPR006133; Stapl/Strept toxin.
Pfam; PF01123; Stap_Strp_toxin; IPR01123; Stap_Strp_toxin; IPR01124; Stap_Strp_toxin; IPR01124; Stap_Strp_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          into phage evolution.";
Genome Res. 13:1042-1155(2003).
BEBL; ARD14161; ARM79908.1; -.
EMBL; AP005142; BAC63655.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.2
Matches 217; Conservative
                                                                                                                        NCBI_TaxID=198466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome
SEQUENCE 251 AA
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Last sequence update)

P62561; P08095; 01-AUG-1988 (Rel. 08, Created) 01-JAN-1990 (Rel. 13, Last seq

STANDARD;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 VSIDGIQSLSFDIETNKKWYTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outbreaks.";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
-!- FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QODPDPSQLHRSSLVKNLQNI YFLYEGDPVTHENVKSVDQLRSHDLI YNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity).

Subunir binds to major histocompatibility complex class II beta chain (By similarity).

SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11917108; DOI=10.1073/pnas.062526099; PubMed=11917108; DOI=10.1073/pnas.062526099; Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S. Sylva G.L., Sturdevant D.B., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M., "Genome sequence and comparative microarray analysis of serotype MIS group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
7
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                                               Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
Exotoxin type A.
By similarity.
54001FE4CCCBFCC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
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0393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00279; BĀCTRLĪOXIN.
PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE009982; AAL97141.1; -.
InterPro; IPR008992; Bact endocox.
InterPro; IPR006137; Bact Lox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Stap/Strept tox.
InterPro; IPR006173; Staph.cx OB.
Pfam; PF02076; Stap Strp tox C; IPR06123; Stap Strp tox C; IPR06123; Stap Strp tox C; IPPEM; Pfam; PF01123; Stap Strp tox C; IPPEM; Pfam; Pfam;
Name=speA; OrderedLocusNames=spyM18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 128 E
251 AA; 29246 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.2%;
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130 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 189
     294 ENFGYNQSVHQINRSDFSKQDWESQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AISTROYNWINILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 AISTROYNWINILPTYSGRESINVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENFGYNÓSVHÓINRSDFSKÓDWEAQIDKELSÓNÓPVYYÓGVGKVGGHAFVIDGADGRNFY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SP268;
MEDLINE-21655126; Pubmed-11796571; DOI-10.1128/IAI.70.2.462-469.2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Jadoun J., Eyal O., Sela S.;
"Role of CsrR, hyaluronic acid, and SpeB in the internalization of Streptococcus pyogenes M type 3 strain by epithelial cells.";
Infect. Immun. 70.462-469(2002).
EMBL; AX035886; AXK71464.1; -.
GO, GO:0008234; F:cysteine-type peptidase activity; IEA.
GO; GO:0006508; P:pyoteclysis and peptidolysis; IEA.
InterPro; IRR000200; Peptidase C10.
Propon; PR00797; STREPOPAIN.
ProDom; PD004169; Peptidase_C10; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.7%; Score 1293.5; DB 2; Length 344; 91.3%; Pred. No. 1.7e-75; tive 5; Mismatches 8; Indels 11;
                                                                                                                                                                                                                                                                                            Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                               354 HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AA; 37345 MW; FB0A9BD05B541909 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Exotoxin type A-phage associated (SpeA precursor).
Name=speA3; OrderedLocusNames=SP80550, SpyM3_1301;
                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
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                                                           DB 1; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN=NZ131;
Watanabe Y., Ohkuni H.;
Watanabe Y., Ohkuni H.;
U. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
R. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
R. GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
R. GO; GO:0006509; P:proteolysis and peptidolysis; IEA.
R. InterPro; IPR000200; Peptidase Cl0.
R. PRINTS; PR00797; STREPTOPAIN.
R. PRINTS; PR00797; STREPTOPAIN.
R. PRODOM; P0004169; Peptidase Cl0; 1.
R. PRODOM; P0004169; Peptidase Cl0; 1.
R. SEQUENCE 398 AA; 43218 WW; 07D1F534E7887CDD CRC64;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
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Last annotation update)
                                                       53.1%; Score 1327.5; DB 1; larity 91.5%; Pred. No. 1.3e-77; Conservative 5; Mismatches 8;
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EMBL; AE006625; AAK34706.1; -. EMBL; AE014170; AAM80349.1; -.
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Best Local Similarity
Matches 257; Conserv
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NCBI_TaxID=1314;
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EMBL;
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   SEQUENCE FROM N.A.
STRAIN=SF370 / ATCC 700294 / Serotype M1;
MEDLINE=211926494; PubMed=11296296; DOI=1073/pnas.071559398;
MEDLINE=211926494; PubMed=11296296; DOI=1073/pnas.071559398;
Ferretti J.G., McShan W.M., Ajdic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
"Complete ganome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hatton M., Hamada S.,
"Genome sequence of an M3 atrain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=MGAS8232 / Serotype M18;
PubMed=11917108; DOI=10.1073/pms.062526099;
PubMed=11917108; DOI=10.1073/pms.062526099;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M., "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=MGAG315 / Serotype M3;
MEDLINE=GAGA315 / Serotype M3;
MEDLINE=21131808; PubMed=12122206; DOI=10.1073/pnas.152298499;
MEDLINE=21131808; PubMed=12122206; DOI=10.1073/pnas.152298499;
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.N., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=76190087; PubMed=1270417; Blliott S.D.; Xortt A.A., Liu T.-Y., Blliott S.D.; Extra J.Y., Kortt A.A., Liu T.-Y., Blliott S.D.; Striptocatal proteinase. III. Isolation of "Primary structure of streptocaccal proteinase. III. Isolation of cyanogen bromide peptides: complete covalent structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY SEQUENCE OF 28-86 AND 121-398.
Yonaha K., Elliott S.D., Liu T.-Y.;
Primary structure of zymogen of streptococcal proteinase.";
J. Protein Chem. 1:317-334(1982).
                                                                     Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                              Hong K.;
"A novel cloning method used arbitrarily primed PCR.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide chain.";
J. Biol. Chem. 251:1955-1959(1976)
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FUNCTION.
STRAIN=NZ131 / Serotype M49,T14;
Microb. Pathog. 15:327-346(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            into phage evolution.";
Genome Res. 13:1042-1055(2003).
                           SEQUENCE FROM N.A.
STRAIN=A-20 / Serotype M1,T1;
                                                                                                                STRAIN=Sv / Serotype M23;
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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outbreaks.";
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                                                                                                              "Streptococcal pyrogenic exotoxin B induces apoptosis and reduces phagocytic activity in U937 cells."; Infect. Immun. 67:126-130(1999).
Kuo C.-F., Wu J.-J., Tsai P.-J., Kao F.-J., Lei H.-Y., Lin M.T., Lin Y.-S.;
                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Preferential cleavage with hydrophobic
                                                                                                                                                                                                                                                                                                                   residues at P2, P1 and P1'.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the peptidase C10 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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AB030578; BAB16027.1; -
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L26130, AAA26997.1;
L26131, AAA26997.1;
L26132, AAA26998.1;
L26133, AAA2699.1;
L26134, AAA27000.1;
L26135, AAA27001.1;
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L26126; AAA26992.1;
L26127; AAA26993.1;
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                                Compugen Ltd.
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Copyright (c) 1993 - 2005 Compug
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ETC1 STAAU
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Q93LQ2
Q8K6K5
SPEA STRP8
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Maximum Match 1008
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2: uniprot_trembl:*
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        32
        487.5
        19.5
        260
        2
        Q79XI4
        Streptococc

        34
        484
        19.4
        264
        2
        Q54739
        GD54739
        Streptococc

        34
        484
        19.4
        264
        2
        Q764P6
        Q764P6
        Q764P6
        GD54739
        Streptococc

        36
        482
        19.3
        259
        2
        Q36G4
        Straphylococ

        37
        478.5
        19.1
        222
        Q6XZE6
        Q6xze7
        Straphylococ

        38
        475.5
        19.0
        222
        Q6XZMS
        Q6xze7
        Straphylococ

        40
        468
        18.7
        261
        Q6XZMS
        Q6xxmS
        Straphylococ

        40
        468
        18.7
        261
        Q6XZMS
        Q6GFNO
        Q6GFNO
        Q6GFNO

        41
        468
        18.7
        261
        2
        Q6XXM3
        Q6xxm3
        Straphylococ

        42
        457
        18.3
        261
        2
        Q6XXM4
        Q6xxm3
        Straphylococ

        44
        445.5
        17.8
        23
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## ALIGNMENTS

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STREAM STREAM STRANDARD, PRT, 1398 AA. GASGER, GASGER,
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enterotoxin D precursor - Staphylococcus aureus
C;Speciess Staphylococcus aureus
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33953
R;Bayles, K.W.; I andolo, J.J.
J Bacteriol. 17, 4799-4806, 1989
A;Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A;Reference number: A33953; MUD:89359112; PMID:2549000
A;Accession: A33953
A;Accession: A33953
A;Accession: A33953
A;Residues preliminary
A;Molecule type: DNA
A;Residues: 1-258 cBAy>
A;Residues: 1-258 cBAy>
A;Residues: 1-258 cBAy>
A;Cross-references: UNIPROT:P20723; GB:MZ8521; NID:g1492109; PIDN:AAB06195.1; PID:g75869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSAC-IGGVTNREGNHLEIPKKIVV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 QLHR----SSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYN---VSGPNYDKLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.8%; Score 295.5; DB 2; Length 258; Best Local Similarity 35.0%; Pred. No. 5e-12; Matches 79; Conservative 44; Mismatches 86; Indels 17; Gaps
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Search completed: September 17, 2005, 01:14:35 Job time : 35.847 secs

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A; Title: Revised sequence of the Porphyromonas gingivalis prtT cysteine protease/hemaggl A; Reference number: Z17199; MUID:95105001; PMID:7806362
A; Accession: T10890
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-886 cMbD>
A; Residues: 1-886 cMbD>
C; Genetics: 1-886 cMbD>
A; Crosser-references: UNIPROT:Q53481; EMBL:S75942; NID:g913136; PID:g913137
C; Genetics: A; Genetics: Gen
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A;Molecule type: DNA
A;Residues: 1-136 <KUR>
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C;Species: Staphylococcus aureus
C;Species: Orday-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89568
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Accession: G89568

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                                                                              Length 266;
                                                                                                                                                                                            70; Indels
                                                                  ; Score 509; DB 1;
; Pred. No. 7.5e-26;
44; Mismatches 70
                                                                        Query Match
Best Local Similarity 44.7%;
Matches 105; Conservative 44
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A;Gene: seg
C;Superfamily: enterotoxin B
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cysteine proteinase (EC 3.4.22.-) / hemagglutinin protein - Porphyromonas gingivalis C; Species: Porphyromonas gingivalis C; Species: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004 C; Accession: T10890 R; Madden, T.E.; Clark, V.L.; Kuramitsu, H.K.

R; Madden, T.E.; Clark, V.L.; Kuramitsu, H.K. Infect. Immun. 63, 238-247, 1995

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A;Cross-references: UNIPROT:Q99T49; GB:BA000018; PID:g13701619; PIDN:BAB42912.1; GSPDB:C-
A;Experimental source: strain N315
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C.; Sekimizu,
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                                                                                                                                                                                                                                                                                                                                                  280 QFADFGSGTFSIFVERALRETFHYKKSLRYIHRSLLPGKEWKOMIRKELAENRPVYYAGA 339
                                                                                                                                                                                                                                                                                                                                                                                                                           KVG-GHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVV 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 DGSMGHAFVCDGYEPDGTFHFNWGWGGMSNGNPYLNLLNPGSLGTGAGDGGYSTDQEVVI 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A89969
C;Accession: A89969
C;Accession: A89969
C;Accession: A9, Minutani-Ui, Y: Kobayashi, I: Baba, T: Yuzawa, H:; Kobayashi, I:, Cui
ma, A.; Minutani-Ui, Y: Kobayashi, N.; Sawano, T:; Inoue, R.; Kaito, C.; Sekii
C:, Shiba, T:; Hattori, M.; Ogasawara, N: Hayashi, H:; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VRNYLLKHKNLYBENSSPYETGYIKFIEGSGHSFWYDLMPESGKKFYPTKYLLIYNDNKT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 ERSACIGGVTNREGNHL-----EIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDF-SQDWEAQIDKELSQNQPVYYQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPE--PEFTQSKYLMIYKDNET
                                                                                                                                                                                                                TYTLSSNNPYFNHPKNLFAA1STRQYNWNN1LPTYSGRESNVQKMA1SELMADVG1SVDM
                                                                                                         230 SKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
                                                   94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
/ Match 16.9%; Score 422; DB 2; Local Similarity 39.0%; Pred. No. 1.8e-19; les 94; Conservative 37; Mismatches 94,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 303.5; DB Pred. No. 6e-13; 3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.1%; Sco
ilarity 47.4%; Pro
Conservative 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::| : :||:|| |
122 VESKSINVEVHLTKK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDSNT-QIEVYLTTK 220
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A;Residues: 1266 <BOH>
A;Cross-references: UNIPROT:P34071
A;Cross-references: UNIPROT:P34071
A;Cross-references: UNIPROT:P34071
A;Accession: B60114
A;Residues: 28-66 <BOH2>
A;Residues: 28-66 <BOH2>
A;Fouch, 71., 4507-4510, 1989
A;Fitle: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests t]
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: P01553; EMBL: X05815; NID: 946566; PIDN: CAA29260.1; PID: 94656'; R; Schmidt, J.J.; Spero, L. J. Biol. Chem. 258, 6300-6306, 1983
A; Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1. A; Reference number: A01816; MUID: 83213327; PMID: 6189824
A; Accession: A01816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene and relatedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterotoxin C-1 precursor - Staphylococcus aureus C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004 C;Accession: S06356; A01816
R;Bohach, G-A.; Schlievert, P.M.
MOI. Genet. 209, 115-20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and 3A;Reference number: S06356; MUID:88038352; PMID:2823067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 QPDPTPDELHKSSEFTGTMGNMKYLYDDHYVSATKVMSVDKFLAHDLIYNISDKKLKNYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 FDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCE-----NAERSACIGGVTNREGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QODPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGYIKFIPKNKESFWFDFFPEP--EFTOSKYLMIYKDNETLDS-NTOIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 510; DB 2; Length 266;
; Pred. No. 6.4e-26;
45; Mismatches 70; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Superfamily: enterotoxin B
C.Keywords: enterotoxin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-1 #status experimental <MAT>
F;120-137/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>
              A; Reference number: A60114; MUID: 89277549; PMID: 2543637
                                                  A;Accession: A60114
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 28-75,'IL',78-176,'N',178-266 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 44.33
Matches 104; Conservative
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A; Residues: 1-266 <BOH>
                                                                                                                       A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S06356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: entCl
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Milternate names: enterotoxin C-3 precursor

C;Species Staphylococcus aureus

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

C;Accession: A60114; B60114; A31866

R;Bohach, G.A.; Schlievert, P.M.

Infect. Immun. 57, 2249-2255, 1999

A;Title: Conservation of the biologically active portions of staphylococcal enterotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Accession: S11885
K.Bovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-33, 1990
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparity A;Accession: S11885, MUD: 90220508; PMID: 2325627
A;Accession: S11885
A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <HOV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P23313; GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C;Superfamily: enterotoxin B
                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SO NVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTEHN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLKTELKNQEMATLFKDKNIDIYGVEYYHLCYLCENA-----ERSACI-GGVTNRE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 FDNGNLQNVLVRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLKTELKNOEMATLFKDKNIDIYGVEYYHLCYLCE-----NAERSACIGGVTNREGNH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 KVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEGNH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
                                                                                                                                                                                                                                                                                                                              QODPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSG---PNYD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETLDS-NTQIEVYLTTKQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                  2 QODPOPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGP---NYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 QPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNISDKKLKNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 16;
                                                                                                                                                Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 266;
                                                                                                                                                                                                                     67; Indels
       F;1-27/Domain: signal sequence #status predicted <SIG>F;28-266/Product: enterotoxin B #status experimental <MAT>F;120-140/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.5%; Score 513; DB 2; L. 45.1%; Pred. No. 4.1e-26; Live 43; Mismatches 70;
                                                                                                                                            21.6%; Score 541; DB 1;
47.7%; Pred. No. 6.3e-28;
ative 39; Mismatches 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enterotoxin C3 - Staphylococcus aureus
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Best Local Similarity 45.18
Matches 106; Conservative
                                                                                                                                                                                                                 Conservative
                                                                                                                                     Query Match
Best Local Similarity
Matches 113; Conserv
F;1-27/Domain: signal
                                                                                                                                                                                                                                                                                                                                                                                                                            28
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9

110 149

89

209

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A;Residues: 1-250 <JOH>
A;Cross-references: UNIPROT:P08095
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
                                                                                                                                                                       Query Match
Best Local Similarity
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C'Species: Streptococcus pyogenes

C'Species: Streptococcus pyogenes

C'Species: Streptococcus pyogenes

A'Variety: strain MGASZ62 isolate California

C'Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004

C'Accession: S18789

R'Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.

J. Exp. Med. 114, 1271-1274, 1991

A;Title: Characterization and clonal distribution of four alleles of the speA gene encod

A;Reference number: S18782; MUID:92044323; PMID:1940804

A;Reference number: S18782; MUID:92044323; PMID:1940804

A;Reference number: S18782

A;Residues: 1-236 <NEL>

A;Residues: 1-236 <NEL

A;Robertics: A;Genetics: A;Geneti
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R;Johnson, D.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to 8
A;Reference number: A26152; MUID:86284313; PMID:3526093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                            BLKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 VSIDGIQSLSFDIETSKKAVTAQELDYKVRKHLTDNKQLYTNGPSKYETGYIKFISKDKE 202
                                                                                                                                                                       VSIDGIQSLSFDIETNKOMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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NiAlternate names: scarlet fever toxin; SPE type A (speA)
C;Species: Streptococcus sp.
C;Species: 10-Sep.1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QODPNPSQLHRSSLVKNLQNIYFLXEGDPVVHENVKSVDQLLSHDLIYNVSGLNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>F;23-236/Product: exotoxin A (fragment) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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88.2%; Pred. No. 6.9e-57;
iive 13; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                       203 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT 233
                                                                                                                                                                                                                                                                                                           181 SFWFDFFPEFFTQSKYLMIYKDNETLDSNT 211
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Matches 186; Conservative
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A;Molecule type: DNA
A;Residues: 1-266 <JON>
A;Cross-references: UNIPROT:P01552; EMBL:M1118; NID:g152999; PIDN:AAA88550.1; PID:g1530
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J. Biol. Chem. 245, 3518-3525, 1970
J. Reference number: A92065; MUID:71007902; PMID:5470821
J. Residues: 28-55, NND', 59-68, NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT', J. Experimental source: strain S-6
R; Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
J. Biol. Chem. 245, 3511-3517, 1970
J. Hich: The primary structure of staphylococcal enterotoxin B. II. Isolation, compositing Reference number: A92064; MUID:71007901; PMID:5470820
J. Contention, L. Poccation, L. Poccat
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Rithung I.Y.; Bergdoll, M.S.

Biol. Chem. 245, 3493-3510, 1970

A;Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, compositic A;Reference number: A92063; MUID:71007900; PMID:5470819

A;Contents: annotation; tryptic peptides

A;Contents: annotation; tryptic peptides

Richantz, E.J.; Resealer, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.

Biochemistry 4, 1011-1016, 1965

A;Title: Purification of staphylococcal enterotoxin B.

A;Reference number: A90648; MUID:66035792; PMID:4953912

A;Reference number: 209, 323-228, 1992

Biochem. 209, 823-288, 1992

A;Title: Identification of functionally active fragments of staphylococcal enterotoxin B.

A;Reference number: S27240; MUID:93049338; PMID:1425690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Staphylococcus aureus
C;Species: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004
C;Date: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004
C;Date: 227360; App-1986
R;Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A;Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A;Reference number: S27360; MUID:86168029; PMID:3957869
A;Accession: S27360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVKVSI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 NQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKVSI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
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                                                                                                                    Gaps
                                                                                                              ä,
                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                    25;
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C;Superfamily: enterotoxin B
C;Keywords: enterotoxin; extracellular protein; toxin
Score 938.5; DB 1
Pred. No. 9.8e-54;
5; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enterotoxin B precursor - Staphylococcus aureus
37.5%;
84.9%;
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                                                                                                                    Matches 185; Conservative
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us-10-002-784a-27.rpr

17

Sep

Sat

strain

enco

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A,Cross-references: EMBL:X61561, NID:g47297, PIDN:CAA43759.1; PID:g47298
A,Experimental source: strain MGAS250 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-236 <NEA>
A; Residues: 1-236 <NEA>
A; Residues: 1-236 <NEA>
A; Cross-references: EMBL:X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A; Experimental source: strain MGAS251 isolate California unassignd phage
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Accession: S18788
A; Status: nucleic acid sequence not shown; translation not shown
                                                                C;Species: Streptococcus pyogenes phage
A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strisolate Winted Kingdom; strain MGAS496 isolate Germany
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S187786; S187787; S18789; S18792; S18795; S18795
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene of the stricts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-236 <NEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S18782; MUID: 92044323; PMID:1940804
A; Accession: S18786
                                     N;Alternate names: scarlet fever toxin
                                                                                                                                                                                                                                                                                                                                                        A; Accession: S18783
A; Status: nucleic acid sequence not shown; translation not shown
A; Accession: S18783
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-236 «NEL»
A; Cross-references: EMBL:X61568; NID:947289; PIDN:CAA43766.1; PID:947290
A; Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A; Accession: S18793
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-236 «NEA.
A; Cross-references: EMBL:X61569; NID:947313; PIDN:CAA43767.1; PID:947314
A; Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A; Accession: S18794
A; Status: nucleic acid sequence not shown; translation not shown
A; Accession: S18794
A; Status: nucleic acid sequence not shown; translation not shown
A; Accession: S18794
A; Status: nucleic acid sequence not shown; translation not shown
A; Accession: S18794
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-236 «NEZ.
A; Cross-references: EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID:947316
A; Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A; Molecule type: DNA
A; Residues: 1-236 «NEZ.
A; Cross-references: EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID:947316
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A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-236 cMED>
A; Cross-references: EMBL:X61571; NID:947323; PIDN:CAA43769.1; PID:947324
A; Experimental source: strain MGAS495 isolate Germany unassigned phage
A; Mcross-references: strain MGAS495 isolate Germany unassigned phage
A; Cross-references: strain MGAS495 isolate Germany unassigned phage
A; Genetics:
A;
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A;Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18801
A;Accession: signal acid sequence not shown; translation not shown
A;Molecule type: DNA
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A.Experimental source: strain MGAS624 isolate Germany unassigned phage
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A,Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text_change 16-Jul-1999 C;Accession: S18783; 3.518794; S18801; S18798 K;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M. J. Exp. Med. 174, 1271-1274, 1991 A;Title: Characterization and clonal distribution of four alleles of the speA gene enc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
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Best Local Similarity 98.6
Matches 208; Conservative
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A,Molecule type: DNA
A,Residues: 1-236 (NEZ>
A,Cross-references: EMBL:X61563; NID:g47301; PIDN:CAA43761.1; PID:g47302
A,Experimental source: strain MGA5256 isolate California unassigned phage
A,Rote: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                             A;Residues: 1-236 (ANEY)
A;Cross-references: EMBL:X61564; NID:g47305; PIDN:CAA43762.1; PID:g47306
A;Cross-references: strain MGAS285 isolate Colorado unassigned phage
A;Experimental source: strain MGAS285 isolate Colorado unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18792
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A;Residues: 1-236 <NEO>
A;Cross-references: EMBL.X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A;Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18795
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A;Cross-references: EMBL:X61566; NID:g47317; PIDN:CAA43764.1; PID:g47318
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A;Rote: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A;Experimental source: strain MGAS496 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
                                                                                                                                                                                                               A;Accession: S18790
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Pred. No. 1.5e-63;
1; Mismatches 3; Indels
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Best Local Similarity 97.6°
Matches 206; Conservative
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exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isol

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A;Residues: 9-244 <NEA>
A;Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292
A;Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292
A;Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigne A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18785
A;Status: nucleic acid sequence not shown; translation not shown
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N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310
A;Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320
A;Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A;Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unass:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294
A;Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned partioner: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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A, Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S18796
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S18797
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S18800
A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; DB 1;
4.4e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: enterotoxin B ; Keywords: exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 9-244 <NEZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 9-244 <NEY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 9-244 <NEO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 9-244 <NEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 9-228 <NES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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N.Alternate names: erythrogenic toxin; scarlet fever toxin
C.Species: Streptococcus pyogenes phage T12
C.Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C.Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
C.Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
R.Wesks, C.R.; Ferretti, J.J.
Infect. Immun. 52, 144-150, 1986
A.Fitle: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g
A.Accession: S29659; MUD:86166804; PMID:3514452
A.Accession: S29659; MUD:86166804; PMID:3514452
A.Molecule type: DNA
A.Molecule type: DNA
A.Reference mumber: S18782; MUD:92044323; PMID:1940804
A.Accession: S18782
A.Accession: S18784
                                                                                                                                                                                                                                              III. Isolation of cyanogen browi
                                                                                       A; Rosidues: 1-337 < YON.
A; Residues: 1-337 < YON.
A; Residues: 1-337 < YON.
B; Tai, J. Y.; Kortt, A.A.; Liu, T.Y.; Elliott, S.D.
J. Biol. Chem. 251, 1955-1959, 1976
A; Title: Primary Structure of streptococcal proteinase. III. Isolation of cyanoge A; Reference number: A00978; MUID: 76190087; PMID: 1270417
A; Accession: A00978; MUID: 76190087; PMID: 1270417
A; Residues: BS-107, L', 109-244, 'N', 246-337 < TAI>
A; Residues: BS-107, L', 109-244, 'N', 246-337 < TAI>
C; Comment: This enzyme can remove the activation peptide from the proenzyme. C; Superfamily: streptococcal cysteine proteinase
C; Keywords: cysteine proteinase; hydrolase; zymogen
F; 1-84/Domain: activation peptide #status experimental < PRO>
F; 131, 279/Active site: Cys, His #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 YLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 NQSVHQIDRGDFSKQDWEAQIDKELSQNQPVYYEGVGKVGGHAFVIDDGAGRNFYHVDWG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YVEQIKENKKLDT-----TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLITPVIEKVKP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 GEQSFVGQAATGHCVATATAQIMKYHNYPDKGLKNYTYTLSSNPDYFDHPKNLFAAISTR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 QYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGY 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 NOSVHOINRSDFS-ODWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFYHVNWG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 GEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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of zymogen of streptococcal proteinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
47.9%; Score 1198; DB 1;
Best Local Similarity 84.1%; Pred. No. 2.2e-70;
Matches 233; Conservative 14; Mismatches 20;
                      A; Reference number: S07668
A; Accession: S07668
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

September 17, 2005, 01:00:14 ; Search time 33.847 Seconds (without alignments) 1330.382 Million cell updates/sec 6

US-10-002-784A-27

2500 1 MQQDPDFSQLHRSSLVKNLQ......ALGTGGGAGGFNGYQSAVVG 468 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

exotoxin type A pr exotoxin type A pr exotoxin type A pr exotoxin A precurs streptococcal pyro enterotoxin B prec enterotoxin YENTZ enterotoxin Dorec enterotoxin SeO [i enterotoxin P [imp extracellular ente enterotoxin SeN [i enterotoxin (3 - S enterotoxin (-2 pr enterotoxin (-1 pr extracellular ente enterotoxin A prec enterotoxin E prec enterotoxin SEM [i extracellular ente enterotoxin Yent1 hypothetical prote hypothetical prote streptococcal pyro streptopain (EC 3. cysteine proteinas exotoxin 11 [impor probable flagellin exotoxin C precurs Description BPSOP S29659 S18783 S18786 S18789 A26152 S11885 A60114 ENSAC1 A33953 E89969 C89984 G89991 H89968 A28664 A28179 D89969 C89969 B89969 H82885 G71609 D89807 G81361 G89968 T10890 489969 Query Match Length DB 136 258 258 258 258 257 257 257 257 257 1327.5 1198 1129 1096.5 1089.5 986.5 303.5 295.5 2091.5 2791.5 262.5 262.5 256.5 256.5 237.5 237.5 183 183 173 134.5 134.5 Score 541 Result Š.

conserved hypothet	hypothetical prote	exotoxin 15 [impor		DNA-directed RNA p	conserved hypothet	zinc metalloprotei	hypothetical prote	rhoptry protein -	hypothetical prote	ORF MSV152 probabl	penicillin-binding	cag pathogenicity	desmocollin 1b pre	desmocollin la pre	Dscla precursor -
F90559	G82885	C89808	B48281	S72284	A89922	H95076	AD1541	T28676	D89991	T28313	S16624	C64588	B48910	A48910	137281
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1183	616	227	1215	960	1146	1881	378	2401	351	1306	675	1186	770	824	840
5.0 1183	4.9 616	4.9 227	4.9 1215	4.9 960		4.8 1881		4.8 2401					4.7 770	4.7 824	4.7 840
2.0	4.9	4.9	4.9	4.9	6.4	4.8		4.8	4.8	4.7	4.7	4.7	4.7	116.5 4.7 824	4.7

### ALIGNMENTS

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RESULT 1
A37768
streptococcal pyrogenic exotoxin type B precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 22-Jun-1999
C;Accession: A3768
R;Hauser, AR.; Schlievert, P.M.
J; Bacteriol. 172, 4536-4542, 1990
A;Title: Nuclectide sequence of the streptococcal pyrogenic exotoxin type B gene and re
A;Reference number: A37768; MUID:90330563; PMID:2198264
A;Accession: A37768
A;Redecole type: DNA
A;Redidues: 1-398 cAAU
A;Redidues: 1-398 cAAU
A;Redidues: 1-398 cAAU
C;Superfamily: streptococcal cysteine proteinase C; Keywords: exotoxin

5 Gaps 11; DB 2; Length 398; 53.1%; Score 1327.5; DB 2; Lengtn 91.5%; Pred. No. 1.1e-78; "\*\*ematches 8; Indels Best Local Similarity 91.5 Matches 258; Conservative Query Match

192 FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI 120 ò 엄

EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308 249 174 δ 임

AISTROYNWNNILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368 AISTRQYNWNNILPTYSGRESNVQXMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 293 234 309 ઠે d

ENFGYNOSVHOINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY 426 ENFGYNQSVHQINKSDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 353 369 294 ò g

HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468 427 ð

354 셤

### RESULT 2

streptopain (EC 3.4.22.10) precursor - Streptococcus pyogenes

Aleternate names: streptococcal cysteine proteinase; streptococcal peptidase A
C;Species: Streptococcus pyogenes
C;Date: 24-Apr-1984 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994
C;Accession: 807668; A00978
R;Yonaha, K.; EJliott, S.D.; Liu, T.Y.
J. Protein Chem. 1, 317-334, 1982

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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               Sequence 13, Application US/09308830
Publication No. US20020086813A1
GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota
TITLE OF INVENTION: MUTANTS OF STREFTOCOCCAL TOXIN A
AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFWFDFFPEPEFTQSKYLMIYKONETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
ADRESSES:
ADRESTED:
ADRESSES:
ADRESTED:
ADRES
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MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-308-830-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 251 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.34
Matches 215; Conservative
US-09-308-830-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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Search completed: September 17, 2005, 01:05:40 Job time : 146.152 secs



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91 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 ELKNQEMATLFKDKAVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                               31 QODPDESQLHRSSLVKNLQNIYFLYEGDEVTHENVKSVDQLLSHDLIXNVSGENYDKLKT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 QQDPDPSQLHRSSLVKKLQNIYFLYEGDPVTHENVKSVDQLLSHHLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                     2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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; Sequence 13, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
APPLICANT: Schlievert, Patrick M.
APPLICANT: Scher, Jennifer
; APPLICANT: Stochr, Jennifer
; APPLICANT: Oblendorf, Douglas
; TITLE OF INVENTION NUMBER: US/08/973,391A
; TITLE OF INVENTION NUMBER: US/08/973,391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR PILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 251;
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                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                DB 16;
                                                                                                                                                                                            Score 1129; DB 16
Pred. No. 3.7e-76;
1; Mismatches 2
                                                           TYPE: PRT
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                            Query Match
Best Local Similarity 97.7%;
Matches 216; Conservative 1
                                                                                                                             US-10-428-817A-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-973-391A-13
                                      LENGTH: 251
SEQ ID NO 163
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOFLASTIC DISEASE
FILE REPERENCE: 38373-189118
CURRENT APPLICATION NUMBER: US 60/378,988
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR PILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-00-01
PRIOR FILING DATE: 2002-10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 BLKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 QQDPDFSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.4%; Score 1136; DB 17; 98.2%; Pred. No. 1.1e-76;
                                                                                                                                                                                                                     ATTORNEY AND THE TOTAL OF THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                        SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
OPERATING SYSTEM: Macintosh 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/438,686
PRIOR FILING DATE: 2003-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 163, Application US/10428817A Publication No. US20040214783A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NOS: 224
PatentIn version 3.2
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Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-767-687-16
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SOFTWARE:

Gaps

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NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles H. Harris
ADBRESSE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
CITY: FORT DETRICK
STATE: MARYLAND
151 VSIDGIQSLSFDIETINKKAVTAQELDYKVRKYLTDNKQLYINGPSKYETGYIKFIPKNKE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 QQDPDF8QLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,QQDPDPSQLHRSSLVKNLQN1YFLYEGDPVTHENVKSVDQLRSHDL1YNVSGPNYDKLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant US-10-002-784A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                               181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                                                                                                 211 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLFTK 251
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REPERENCE: 003/233/SAP
CURRENT PELICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 16
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 SFWFDFFFPEFFTQSKYLMIYKONETLDSNTSQIEVYLTTK
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Pred. No. 1.1e-76;
1; Mismatches 1;
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Mark A. OIGON
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
                                                                                                                                                                                                                                                                  ; Sequence 16, Application US/10002784A; Publication No. US20030036644A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
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Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.2%
Matches 217, Conservative
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                                                                                                                                                                                                                     RESULT 11
US-10-002-7,84A-16
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US-10-767-687-16
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Publication No. US2030009015A1
Sequence 16, Application US2030009015A1
Sequence 16, US2030009015A1
SEGENBAL INPORMATION:
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
ITILE OF INVENTION: Vaccines
NUMBER OF SEQUENCES:
ADDRESSED: John Moran
STREET: US Army MRWC -504 Scott Street MCWR-JA (John Moran-Patent Atty)
STREET: US Army MRWC -504 Scott Street MCWR-JA (John Moran-Patent Atty)
STREET: US Army MRWC -504 Scott Street MCWR-JA (John Moran-Patent Atty)
STREET: US Army MRWC -504 Scott Street MCWR-JA (John Moran-Patent Atty)
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STREET: US Army MRWC -504 Scott Street MCWR-JA (John Moran-Patent Atty)
STREET: US Army MRWC -504 Scott Street MCWR-JA MACINCOSH MCAINCOSH (John MCAINCOSH ATT)
MEDIUM TYPE: Floppy disk
COMPUTER: MACINCOSH MCAINCOSH / STREET MCAINCOSH MCAINCOSH / STREET MCAINCOSH MCAINCOSH / STREET MCAINCOSH MCAINCOSH / STREET MCA
                                                   TELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIGGVTNREGNHLEIPKKIVVK 120
                                                                                                                                     180
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                                                                                                                               VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE
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1; Mismatches
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Matches 217; Conservative
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Length 251;

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LENGTH: 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 EKVKPGEQSFVGQHAATGSVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 AISTRQYNWNNILPTYSGRESNVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY 426
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US-11-021-951-25

i Sequence 25, Application US/11021951

publication No. US20050175581A1

i GENERAL INPORMATION:

APPLICANT: HAUPTS, Ulrich

APPLICANT: KOLTERMANN, Andre

APPLICANT: SCHEIDIG, Andreas

APPLICANT: COCO, Wayne Michael

TITLE OF INVENTION: New Biological Entities And The Pharmaceutical

TITLE OF INVENTION: New Biological Entities And The Pharmaceutical

TITLE OF INVENTION: New Biological Entities CURRENT APPLICATION NUMBER: US/11/021,951

CURRENT FILING DATE: 2004-12-22

PRIOR FILING DATE: 2004-06-18

PRIOR FILING DATE: 2004-06-18

PRIOR FILING DATE: 2004-06-18
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            Sequence 25, Application US/10872197A
Sequence 25, Application US/10872197A
Sequence 25, Application No. US20050059126A1
GENERAL INFORMATION:
APPLICANT: Andrea SCHEIDIG
APPLICANT: Andreas SCHEIDIG
APPLICANT: Andreas SCHEIDIG
APPLICANT: Ulrich KETTLING
APPLICANT: Ulrich KETTLING
APPLICANT: Ulrich KETTLING
APPLICANT: Ulrich KETTLING
CURRENT APPLICATION NUMBER: US/10/872,197A
CURRENT APPLICATION NUMBER: 2004-06-18
FILE REFERENCE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
SROFTWARE: PatentIn version 3.1
SEQ ID NO 25:
LENGTH: 371
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Pred. No. 6e-90;
4; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.1%;
Matches 257; Conservative
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US-10-872-197A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A US-10-002-784A-26
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TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.7%; Score 1316.5; DE 91.1%; Pred. No. 6e-90; cive 4; Mismatches 1
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: BP 04003058
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2004-02-11
PRIOR FILING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: BP 03025851
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-11-10
PRIOR FILING DATE: 2003-10-18
NUMBER OF SEQ ID NOS: 191
SOFTWARE: Patentin Version 3.1
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 26, Application US/10002784A; Publication No. US20030036644A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pyogenes US-11-021-951-25
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ORGANISM: Artificial sequence
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Matches 257; Conservative
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294 ENFGYNQSVHQINRGDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY 426
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                                                                 234 AISTRÒYNWINILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK
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                                                                                                                               ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
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APPLICANT: Andreas SCHEIDIG
APPLICANT: Andreas SCHEIDIG
APPLICANT: Andreas SCHEIDIG
APPLICANT: Christian VOETSMEIER
APPLICANT: Ulrich Kettling
ITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REFERENCE: 04156.000204
CURRENT APPLICATION NUMBER: US/10/872,198
CURRENT FILING DATE: 2004-06-18
FRICH REPLICATION NUMBER: 60/543,518
FRICH RELING DATE: 2004-02-11
FRICH APPLICATION NUMBER: EP 04003058
FRICH APPLICATION NUMBER: EP 04003058
FRICH APPLICATION NUMBER: EP 04003058
FRICH APPLICATION NUMBER: EP 03025871
FRICH RILING DATE: 2003-11-10
FRICH RILING DATE: 2003-11-11
FRICH APPLICATION NUMBER: EP 03025851
FRICH APPLICATION NUMBER: EP 03013819
FRICH FILING DATE: 2003-11-10
FRICH FILING DATE: 2003-10-11
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; Sequence 25, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
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US-10-872-198-25
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                                                                                                                                                                                                                                                                                           95 ERSACI-GGVTNREGNHLEIPKKIVVKVSIDGIQSLSFDIETNK-KMVTAQELDYKVRKY 152
                                                                                                                                                                                                                                                                                                                         195 TATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRES 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 LTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEFFTQSKYLMIYKDNETLDSNTQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                            104 STSG----SFDANGKENI-----ASFMES-YVEQIKENKKLDT--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 IEVYLTT---KOPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 --TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKFGEQSFVGQHAATGCVA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRES 329
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                                                                                                                     ; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin B prosegement US-10-002-784A-24
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                                                                                                                                                                                                                                                   39; Gaps
                                                                                                                                                                                              Query Match 53.0%; Score 1324.5; DB 14; Length 398; Best Local Similarity 71.7%; Pred. No. 1.7e-90; Matches 273; Conservative 20; Mismatches 49; Indels 39;
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APPLICANT: Olmsted, Stephen
APPLICANT: Zagursky, Robert
APPLICANT: Wickbarg, Biliot
APPLICANT: Winter, Lourie
ITILE OF INVENTION: SURPACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
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Publication No. US20040236072A1
GENERAL INFORMATION:
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                                                                        ORGANISM: Artificial sequence
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SEQ ID NO 24
LENGTH: 398
TYPE: PRT
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LENGTH: 398
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266

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Length 371;

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Sequence 164, Application US/10428817A
Publication No. US20040214783A1
                 US-10-428-817A-164
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ORGANISM:
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                   121 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                  300
                                                                                                                                                                                                                         241 YNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYF 300
                                                                                                                                                                                                  NHPKNLFAAISTRQYNWNNILPTYSGRESNVQKWAISELMADVGISVDMDYGPSSGSAGS 360
                                                                                                                                                                                                                                                                                                    361 SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQNQPVYYQGGKVGGHAFVIDGA 420
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                                                                                    181 SFWFDFFFDEDEFTQSKYLMIXKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
                                                                                                                                                    241 YNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYF
                                                                                                                                                                                                                                                                    SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQNQPVYVQGGKVGGHAFVIDGA
                                                                  SFWFDFFPBPFFTQSKYLMIYKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-B US-10-002-784A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APJICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERRICE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR PILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 25
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.3%; Score 1332; DB 14;
100.0%; Pred. No. 2.4e-91;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-10-002-784A-25
Sequence 25, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.3%
Best Local Similarity 100.0
Matches 248; Conservative
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PRIOR PRILICATION NUMBER: US 60/415,310
PRIOR PILLICATION NUMBER: US 60/415,310
PRIOR PILLICATION NUMBER: US 60/415,310
PRIOR PILLING DATE: 2002-06-15
PRIOR PILLING DATE: 2002-06-29
PRIOR PILLING DATE: 2002-06-29
PRIOR PILLING DATE: 2002-06-29
PRIOR PILLING DATE: 2002-06-29
PRIOR PILLING DATE: 2002-10-01
PRIOR PILLING DATE: 2002-10-01
PRIOR PILLING DATE: 2002-10-01
PRIOR PILLING DATE: 2002-10-01
PRIOR PILLING DATE: 2002-10-02
PRIOR PILLING DATE: 2002-10-03
PRIOR PILLING DATE: 2002-10-03
PRIOR PILLING DATE: 2002-10-03
PRIOR PILLING DATE: 2003-01-09
PRIOR PILLING DATE: 2003-01-09
PRIOR PILLING DATE: 2003-01-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 AISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENFGYNOSVHOINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
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CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/682,41; 09/144,776
PRIOR FILING DATE: 99-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
53.1%; Score 1327.5; DE
Best Local Similarity 91.5%; Pred. No. 1e-90;
Matches 258; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Streptococcus pyogenes US-10-428-817A-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin version 3.2
SEQ ID NO 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-10-002-784A-24
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Sequence 27, Appl
Sequence 25, Appl
Sequence 164, Appl
Sequence 642, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 16, Appl
Sequence 16, Appl
                                                                                                                           September 17, 2005, 00:44:58; Search time 145.152 Seconds (without alignments) 1305.574 Million cell updates/sec
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                                                                                                                                                                                                                                                              1 MQQDPDPSQLHRSSLVKNLQ.....ALGTGGGAGGFNGYQSAVVG 468
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| Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-002-784A-25
US-10-002-784A-24
US-10-002-784A-24
US-10-474-792-642
US-10-474-792-642
US-10-872-197A-25
US-10-951-25
US-10-002-784A-26
US-10-002-784A-16
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                                                                                                                                                                                                                                                                                                                                                                            1812044 segs, 404927589 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                  using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2500
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Sequence 16, Appl Sequence 13, Appl Sequence 13, Appl Sequence 20, Appl Sequence 20, Appl Sequence 16, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 10, Appl Sequence 6, Appli Sequence 6, Appli Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 14, Appl Sequence 16, Appl Sequence 185, Appl Sequence 11, Appl Sequence 185, Appl Sequen	a)
US-10-767-687-16 US-10-428-817A-163 US-09-308-830-13 US-09-308-830-13 US-09-870-759-20 US-09-870-759-20 US-09-870-759-20 US-10-937-758A-20 US-09-150-947B-12 US-10-947B-12 US-10-947B-12 US-10-947B-12 US-10-947B-12 US-10-947-758A-10 US-09-751-708A-10 US-09-751-708A-10 US-09-751-708A-10 US-10-152-817A-6 US-10-152-817A-6 US-10-152-817A-6 US-10-152-817A-6 US-10-152-817A-6 US-10-152-817-6 US-10-152-817-6 US-10-152-817-6 US-10-152-817-6 US-10-152-817-6 US-10-152-817-14 US-10-152-817-14 US-10-152-817-186 US-10-152-817-186 US-10-428-817A-186 US-10-428-817A-186 US-10-428-817A-186 US-10-428-817A-185 US-10-923-324-1	US-09-751-708A
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## ALIGNMENTS

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TELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIGGYTNREGNHLEIPKKIVVK 120
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0
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                                                                                             /33

APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/803,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40

SOFTWARE: Apple Macintosh Microsoft Word 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion US-10-002-784A-27
                      Sequence 27, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468; Conservative
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Best Local Similarity
JS-10-002-784A-27
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 27
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58 KLKTELKNOEMATLFKDKNIDIYGVEYYHLCYLCENA-----ERSACI-GGVTNRE 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 QPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYD
                                                                                                                                                                                                                                                                   2 QODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGP---NYD
                                                                                                                                                                          Query Match 21.6%; Score 541; DB 1; Length 255; Best Local Similarity 47.7%; Pred. No. 1.1e-39; Matches 113; Conservative 39; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: September 17, 2005, 00:48:31 Job time: 27.0362 secs
                                          : 255 amino acids
amino acid
GY: linear
INFORMATION FOR SEQ ID NO:
                     SEQUENCE CHARACTERISTICS LENGTH: 255 amino acio
                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-918A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 PKPSQLQRSNLVKTFKIYIFFMRVTLVTHENVKSVDQLLSHDLIYNVSGPNYDKLKTELK 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.5%; Score 938.5; DB 4; Length 220; 84.9%; Pred. No. 5.5e-75; ive 5; Mismatches 25; Indels 3
         GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTICENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/09/708,008B
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US/28/978
PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE FASTESQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: 0010rado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 220
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REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pyogenes
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(303) 863-0223
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ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
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Best Local Similarity 84.99
Matches 185; Conservative
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                                                                                                                                                    64 NQEMATLFKDKNVDIYGVEYYHLCYLCENABRSACLYGGVTNHEGNHLEIPKKIVVKVSI 123
                                                                                                                                                                                                                          124 DGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 183
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                            PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKTELK
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Pred. No. 5.5e-75;
5; Mismatches 25;
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CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING BATE: 1999-05-18
EARLIER APPLICATION NUMBER: US/09/313
EARLIER FILING DATE: 1997-07-18
EARLIER FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/25,978
EARLIER FILING DATE: 1997-06-01
EARLIER APPLICATION NUMBER: US/09/34
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1990-01-17
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US-09-708-008B-20
; Sequence 20, Application US/09708008B
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Best Local Similarity 84.9%;
Matches 185; Conservative
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APPLICANT: Terman, David S.
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US-09-314-235-20
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                                                                                                               Sequence 13, Application US/08973391C

Patent No. 6632441

GENERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
APPLICANT: Schlievert, Jennifer

APPLICANT: Stock, Jennifer

APPLICANT: Stock, Jennifer

APPLICANT: Oblendorf, Douglas

TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE

TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE

TITLE REPERENCE: 600-3112WO

CURRENT APPLICATION NUMBER: US/08/973,391C

CURRENT APPLICATION NUMBER: US 08/480,261

PRIOR APPLICATION NUMBER: US 08/480,261

PRIOR PILING DATE: 1995-06-07

PRIOR PILING DATE: 1995-06-07

WUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.1
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APPLICANT: Terman, David S.
TITLE OF INVENTION: TUNOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: TUNOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
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181 SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLITK 221
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84.9%; Pred. No. 5.5e-75;
cive 5; Mismatches 25;
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Best Local Similarity 97.3%;
Matches 215; Conservative
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Best Local Similarity 84.9
Matches 185; Conservative
                                                                        RESULT 11
US-08-973-391C-13
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US-08-896-933-20
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LENGTH: 251
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VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                                                                                   44.9%; Score 1123; DB 3; Length 221; 97.3%; Pred. No. 2.6e-91;
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                         181 SFWFDFFFFFFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
                                         SFWFDLFPEPEFTQSKYLMIYKONETLDSNTSQIEVYLTTK 221
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                                                                                                                Sequence 29, Application US/09314235 Patent No. 6338845
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Matches 215; Conserv
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                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Roggiani, Manuela APPLICANT: Roggiani, Manuela APPLICANT: Stochr, Jennifer APPLICANT: Stochr, Jennifer APPLICANT: Obuglas TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE FILE REFERENCE: 600.3110SWO CURRENT APPLICATION NUMBER: US/08/973,391C CURRENT APPLICATION NUMBER: US/08/973,391C CURRENT APPLICATION NUMBER: US/08/973,391C PRIOR FILING DATE: 1996-06-07 PRIOR FILING DATE: 1996-06-07 PRIOR FILING DATE: 1996-06-07 NUMBER OF SEQ ID NOS: 14 SOFTWARE PARENT PARENT NOS: 14
                                                                                                                                                                                                                                                                                                                                                                               1 QODPDPSQLHRSSLVKNLQNIYELYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SFWFDLFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 221
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                                                                                                                                                                                                                                          Score 1123; DB 4;
Pred. No. 2.6e-91;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1122; DB 4;
Pred. No. 3.2e-91;
1; Mismatches 3;
PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 14, Application US/08973391C; Patent No. 6632441
                                                                                                                                                        ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Schlievert, Patrick
APPLICANT: Roggiani, Manuela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.9%;
al Similarity 97.3%;
215; Conservative 1
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.3%;
Matches 215; Conservative
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Best Local Similarity
Matches 215; Conserv
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121 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: THE APPLICANT: TERMIN, David S.

TITLE OF INVENTION: TUMOR KILLING BEFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFWFDFFPEPEFTQSKYLMIYKDNETLDSNT-QIEVYLTTK 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1136; DB 4;
Pred. No. 2.2e-92;
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Patent No. 6221351
GENERAL INFORMATION:
                                                  NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptococcus pyogenes
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FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.2<sup>3</sup>
Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Unknown; MOLECULE TYPE: Peptide US-08-882-4318-16
                                                                                                                                                                                                                                                                                                                                                 TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QODPDFSQLHRSSLVKALQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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                    FILING DATE: 01-Sep-1998
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION UNDBER: 34,616
REFERENCE/DOCKET NUMBER: <UNKnown>
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAK: (301) 619-2065
TELEPAK: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/09/144,776B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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Matches 217; Conservative
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REGISTRATION NUMBER: 32,750
REBERBROKE MOCKET NUMBER: BAYL-004/02US
TELECOWUNICATION INFORMATION:
TELEPAN: (415) 926-6200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
PRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
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CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
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                                                                                                                                                                                                                LENGTH: 398 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: MGAS 1719 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US96-05997-1
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US-09-144-776B-16
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Sequence 1, Application PC/TUS9605997

GENERAL INFORMATION:

APPLICANT: Manchaswamy, H. N.

APPLICANT: Repur M.D., Vivek

APPLICANT: Ferrandez, A.

TITLE OF INVENTION: Use of extracellular cysteine protease

TITLE OF INVENTION: to inhibit cell proliferation

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: WEIL, GOTSHAL & MANGES

STREET: 2882 Sand Hill Road, Suite 280

CITY: Menlo Park

STATE: CA.

COUNTRY: USA.
                                                                                                                                                                                                                                                                                                                                                              Indels 11;
                                                                                                                                                                                                                                                                                                                       Query Match 53.1%; Score 1327.5; DB 5; Length 398; Best Local Similarity 91.5%; Pred. No. 5.1e-109; Matches 258; Conservative 5; Mismatches 8; Indels 11;
AUTHORS: Hamrick, M. R.

AUTHORS: Hamil, R. J.

AUTHORS: Patti, J. M.

AUTHORS: Musser, J. M.

TITLE: A conserved Streptococcus pyogenes

TITLE: extracellular cysteine protease cleaves human

TITLE: fibronectin and degrades vitronectin

OUUNMAL: Microb. Pathog.

PAGES: 327-346

DATE: 1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,542
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/160,965
FILING DATE: 02-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter Ph.D., Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: PCT/US96/05997
01-MAY-1995
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249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
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                                                                         11;
          Length 398;
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          DB 5;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US ARMY MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Query Match 53.1%; Score 1327.5; DB 5
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8;
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Topouzis, S.
Majesky, M. W.
Li, L. - L.
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MEDIUM TYPE: Floppy
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Betent No. 6833262
GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN FILE REFERENCE: 235.00210201

CURRENT APPLICATION NUMBER: US/10/030,330

CURRENT FILING DATE: 1999-04-19

PRIOR APPLICATION NUMBER: 60/130,436

PRIOR APPLICATION NUMBER: 60/130,436

PRIOR SEQ ID NOS: 6

SOFTWARE: PATENTIN Ver. 2.1

SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 11; Gaps
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                                                                    AUTHORS: Kapur, V.
AUTHORS: Topouzis, S.
AUTHORS: Majesky, M. W.
AUTHORS: Li, Li- L.
AUTHORS: Hamil, R. J.
AUTHORS: Patti, J. M.
AUTHORS: Maser, J. M.
AUTHORS: Muser, J. M.
AUTHORS: Muser, J. M.
TITLE: A conserved Streptococcus pyogenes
TITLE: Atracellular cysteine protease cleaves human
TITLE: fibronectin and degrades vitronectin
JOURNAL: Microb. Pathog.
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STRAIN: MGAS 1719
IMMEDIATE SOURCE:
CLONE: SPEB7 (cysteine protease)
PUBLICATION INFORMATION:
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Matches 258; Conservative
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DATE: 1993
US-08-931-220-5
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-10-030-330-6
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-030-330-6
PCT-US95-11723-5
PCT-US96-05997-1
US-09-144-7768-16
US-09-314-23-29
US-09-314-23-29
US-09-973-391C-13
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US-08-974-7768-6
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US-09-144-776B-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 FTQSKYLMIYKDNETLDSNTQIEVYLTT----KQPVVKSLLDSKGIHYNQGNPYNLLTFVI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 XISTRQYNWNNILPTYSGRESNVQKWAKSELMADVGISVDMDXXPSSGSAGSSRVQRALX 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 AISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
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                                                                                                                                                                                                                                         Novel oral bacterial periodontain polypeptide for treating periodontal diseases, has amidolytic activity for cleavage of non-denatured human alphal-proteinase inhibitor at reactive site loop region of inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.8%; Score 1195.5; DB 3; Length 398; 84.0%; Pred. No. 1.3e-88; Live 5; Mismatches 29; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
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                                                                     (UYGE-) UNIV GEORGIA RES FOUND INC.
(FOTAV) TRAVIS J.
(FOTE/) POTEMPA J.
(NELS/) NELSON D.
                                                                                                                                                                    Nelson D;
                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1; 55pp; English
20-APR-2000; 2000WO-US010574.
                                     99US-0130436P
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                                                                                                                                                                  Travis J, Potempa J,
                                                                                                                                                                                                      WPI; 2000-679600/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 398 AA;
                                 21-APR-1999;
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hyperimmune serum reactive antigen or its fragment from Streptococcus pyogenes. The nucleic acid molecule or hyperimmune serum-reactive antigen or its fragment from Streptococcus or its fragment are useful for the manufacture of a pharmaceutical preparation, especially a vaccine, against S. pyogenes infection. In addition, the hyperimmune serum reactive antigen or fragment is used for the isolation and/or purification and/or identification of an interaction partner of the hyperimmune serum reactive antigen or its fragment, for the generation of a poptide (e.g. anticalines) binding to the antigen or fragment, or for the manufacture of a functional nucleic acid selected fragments and spiegelmers. The nucleic acid molecule may also be used for the manufacture of functional ribonucleic acids such as ribozymes, antisense nucleic acids and siRNA. ADR83733-ADR84189 represent S. pyogenes hyperimmune serum reactive antigens, fragments and the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AISTRQYNWINILLPTYSGRESNVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid molecules encoding hyperimmune serum-reactive antigens from Streptococcus pyogenes, useful for diagnosing, preventing and treating S. pyogenes infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTQSKYLMIYKDNETLDSNTQIEVYLTT----KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superantigen toxin; vaccine; infection; pyrogenic exotoxin B; SpeB;
                                                                                                                                       invention describes a novel nucleic acid molecule encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.9%; Score 1323.5; DB 8; Length 398; larity 91.1%; Pred. No. 4.6e-99; Conservative 5; Mismatches 9; Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide described in the invention
                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                               Claim 14; SEQ ID NO 239; 145pp;
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les 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 398 AA;
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10-JUL-2003

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                                                                                                                                                                                                                                                        The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes mature pyrogenic exotoxin B (SpeB) mutant protein. This sequence is used in the invention. Note: This sequence is not shown in the specification, but is derived from S. pyogenes mature wild-type SpeB protein (AAE37686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                            New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1322; DB 7;
Pred. No. 3.1e-99;
                                                                             (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 398 AA.
                                                                                                                                                                                                                            Claim 42; Page; 141pp; English.
                                               26-NOV-2001; 2001US-00002784.
               26-NOV-2001; 2001WO-US046540
                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.9%;
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Matches 247; Conservative
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                                                                                                                                              WPI; 2003-492125/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 248 AA;
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                                                                                                               Ulrich RG;
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WPI; 2003-492125/46.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 AISTROYNWNNILPTYSGRESNVOKWAISELMADVGISVDMDYGPSSGSAGSSRVOKALK 293
          activity. [1], nucleic acids encoding [1], ABN66044-ABN71526 and antibodies that bind [I] are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding [I] are used to detect Streptococcus in a biological sample. [I] is used to detectmine whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce [I] and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
antibacterial and antiinflammatory
                                                                                                                                                                                                                                                                                                             FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
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                                                                                                                                                                                                                                                    DB 5; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes pyrogenic exotoxin B (SpeB) protein
                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395
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                                                                                                                                                                                                                                                                   Pred. No. 4.6e-99;
                                                                                                                                                                                                                                                    Score 1323.5;
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/label= Signal_peptide
146. .398
 The proteins have
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91.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin B (SpeB) protein. This sequence is used in the
                                               superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                RKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
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                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                           Length 398;
                                                                                                                                                                                                                                                                                     9; Indels
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    S. pyogenes hyperimmune system reactive antigen Spy2039.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                             DB 7;
                                                                                                                                                                                                                                                             Score 1323.5; DB Pred, No. 4.6e-99;
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                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                      Example 14; Page 133; 141pp; English
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                                                                                                                                                                                                                                                             52.9%;
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N-PSDB; ADR83821.
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Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyrogenic enterotoxin a; vaccine; superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.0%; Score 1124.5; DB 7; Length Best Local Similarity 71.7%; Pred. No. 3.8e-99; Matches 273; Conservative 20; Mismatches 49; Indels
                                HINNEWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395
                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyrogenic toxin b, wild-type pro-sequence.
HVNWGWGGVSDGFFRLDALNPSALGTGGGGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 14; Page 40-42; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 .145
/label=_Pro_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146. 398 // label= Mature_SPEb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                             ABU62332 standard; protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-NOV-2001; 2001US-00002784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-00882431
98US-00144776
                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ULRI/) ULRICH R G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1997;
01-SEP-1998;
                                                                                                                                                                                                                                                                                                           27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ulrich RG;
427
                                                 354
                                                                                                                                                                                                                                                    ABU62332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
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10;

Gaps

39;

DB 7; Length 398;

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
                                   47 OKSAAİKAGARSAEDIKLD---KVNLGGELSGSNMYGYNİSTGGFVIVSGDKRSPEILGY 103
                                                                                                                                                                                                                                329
                                                                                                                                                                                                                                                                                                         388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
95 ERSACI-GGVTNREGNHLEIPKKIVVKVSIDGIQSLSPDIETNK-KMVTAQELDYKVRKY 152
                                                                                                                                                                                                                                                                                                                                             314
                                                                                                                                                                                                                                                                                                                                                                                   389 WEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNP 447
                                                                                                                                                                                                                                                                                                                                                                                                       315 WEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                               137 --TYAGTAEIKQPUVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVA
                                                                                                                                                                                                                                                    195 TATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRES
                                                                                                                                                                                                                                                                                                                                     255 NVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRGDFSKQD
                                                                         153 LTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSNTQ
                                                                                                                                                  213 IEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVA
                                                                                                                                                                                                                              270 TATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRES
                                                                                                                                                                                                                                                                                                         NVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFS-QD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masignani V, Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus polypeptide SEQ ID NO 8334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 3948; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 SALGTGGGAGGFNGYQSAVVG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALGTGGGAGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP29579 standard; protein; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-2001; 2001WO-GB004789.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-352536/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABN70210.
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26-FEB-2004
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              ADF89840;
엄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the S. pyogenes cysteine protease speB7. The invention relates to a method for determining the presence of a Group A Street which expresses an extracellular protease (preferably speB) capable of degrading proteins of the extracellular matrix, comprising:

(1) combining a sample with an assay medium comprising a first member of a specific binding pair which binds to a second member of the binding pair which binds to a second member of the binding pair where the first member has at least 1 epitopic site competitive with at least 1 conserved epitopic site on the protease; and (2) detecting complex formation as indicative of the presence of the patence of infection with Streptococcus pyogenes and for monitoring the disease status of the host. The speB gene products are used as a vaccine for protecting against Streptococcus mediated diseases such as for protecting against Streptococcus mediated diseases such as paryngitis, tonsillitis, skin infections, scarlet fever, sepsis, erysipelae, fascilitis, pneumonia, acute rheumatic fever, sepsis, erysipelae, fascilitis, pneumonia, acute rheumatic fever, sepsis, and
                                                                                                                                                                                                                                                                                                                               Determining the presence of a Group A Streptococcus expressing a protease capable of degrading proteins of the extracellular matrix, using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 FMES-YVEQIKENKKLDT----TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AISTROYNWNNILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTOSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.1%; Score 1327.5; DB 3; Length ilarity 91.5%; Pred. No. 2.2e-99; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Col 7-8, 56pp, English.
                                                                                                                                                                                                    BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                   93US-00160965.
94US-00306542.
                                                                                                                    97US-00931220
                                                                                                                                                                                                                                          Musser JM;
                                                                                                                                                                                                                                                                           WPI; 2000-205208/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
tes 258; Conserv
                                                                                                                                                                                                                                                                                                                                                                  specific antibody.
                                                                                                                                                                                                                                                                                           N-PSDB; AAA07111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 398 AA;
                                                                                                                  16-SEP-1997;
                                                                                                                                                     02-DEC-1993;
                                                                                                                                                                     14-SEP-1994;
                                                 US6030835-A
                                                                                 29-FEB-2000
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                                                                                                                                                                                                                                          Kapur V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
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ADF89840 standard; protein; 398

ADF89840 ID ADF8 RESULT 9

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The invention relates to treating a subject with cancer. The method involves administering an amount of a superantigen (SAg) composition comprising a molecule selected from: a native SAg protein; its biologically active fragment or a native SAg protein; its biologically active fragment or comprising the SAg or its fragment or homologue fused to a fusion protein comprising the SAg or its fragment or homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating a subject with cancer or malignant diseases comprises intratumoral, intrathecal or intracavitary administration of an amount of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AISTROYNWINILPTYSGRESNVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents a Streptococcal pyrogenic exotoxin B (SpEB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 FMES-YVEQIKENKKLDT----TYAGTAEIKOPVVKSLLDSKGIHYNGGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 FTQSKYLMIYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                     enterotoxin; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8; Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                            Streptococcal pyrogenic exotoxin B (SpEB) sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1327.5; DB
Pred. No. 2.2e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               superantigen composition to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 17; 91pp; English
                                                                                                                 Superantigen; SAg; enterotoxir
pyrogenic exotoxin; SpE; SpEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002, 2002US-0389366P.
28-AUG-2002, 2002US-0406697P.
29-AUG-2002, 2002US-0405750P.
01-OCT-2002, 2002US-0415310P.
02-OCT-2002, 2002US-0415400P.
                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2003; 2003WO-US014381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002US-0378988P.
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91.5%;
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-011997/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TERM/) TERMAN D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 258; Conserv
                                                                                                                                                                                                                βĎ.
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                                                                                                                                                                                                                                                                      WO2003094846-A2
                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2002;
                                                                                                                                                                                                                                                                                                                                  20-NOV-2003
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The present sequence is the Streptococcus pyogenes clone speB7 pre-pro cysteine protease (CP), which can be used to inhibit neoplastic cell proliferation, especially in a human, useful in the treament of neoplastic conditions, e.g. carcinomas, sarcomas, melanomas, lymphomas and leukaemias originating from blood, lung, mammary gland, prostate, intestine, stomach, liver, heart, skin, pancreas or brain tissue. The CP is especially associated with a wound covering, and can also be used to prevent metastasis or identify susceptible neoplastic cells. K1735 and CM519 melanoma cells were injected s.c. into nu/nu mice, optionally followed by i.p. injection of CP (100 microg, 24 hours later). The mice were checked twice weekly for tumour growth for 12 weeks, to give results that showed that treatment with CP completely protected athymic mice against transplanted K175 melanoma growth, and protected 60% of the mice
                                                                                                                                                                                                                                                                                                                                                                                                               248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody; vaccine; diagnosis; detection; Streptococcus infection; group A; prevention; treament; pharyngitis; tonsillitis; skin infection; acute rheumatic fever; scarlet fever; probe; post-streptococcal glomerulonephritis; sepsis; meningitis; erysipelis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353
                                                                                                                                                                                                                                                                                                                                                                                                                                      120 FMES-YVEQIKENKKLDT-----TYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide; speB gene; extracellular protease; production;
                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                        DB 2; Length 398;
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/label= putative nucleotide binding domain
382. .398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= potential collagen docking region
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468

    S. pyogenes speB gene encoded extracellular protease.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "corresponding codon TAG" 333. .338
                                                                                                                                                                                                                                                                                                                                 53.1%; Score 1327.5; DB :
llarity 91.5%; Pred. No. 2.2e-99;
Conservative 5; Mismatches 8
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                                                                                                                                                                                                                                                              from developing CM519 melanomas
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 258; Conserv
                                                                                                                                                                                                                                                                                                Sequence 398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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21-MAR-1996

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                                                                                                                                                                                                                                                                                                                     The present sequence is the S. pyogenes speB gene encoded extracellular protease. An immunogenic peptide derived from the protease can be used in the prodn. of antibody (Ab) and vaccine. Ab is prepd. by introducing the peptide into a mammal, pref. a mouse, followed by Ab isolation. The Ab or a probe derived from the gene can be used for the diagnosis and detection of gp. A Streptococcus infections, while vaccine, which inhibits streptococcus infections, and be used to prevent and treat gp. A Streptococcus infections, and partic. to ameliorate pharyngitis, to sillifis, skin infections, acute rheumatic fever, scarlet fever, post-streptococcus glomerulonephritis, sepsis, meningitis, erysipelis, cellulitis, fasciitis and toxic shock like syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AISTRQYNWNNILPTYSGRESNVQKWAISELMADVGISVDMDYGPSSGSAGSSRVQRALK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNQPVYYQG-GKVGGHAFVIDGADGRNFY 426
                                                                                                                                                                                                             Use of extracellular protease(s), partic. cysteine protease - for detection, diagnosis prevention and treatment of infection by pathogenic organisms, partic. gp. A streptococcus strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cysteine protease; speB; Group A Streptococcus; extracellular protease; detection; diagnosis; extracellular matrix; infection; skin infection; disease status monitoring; vaccine; Streptococcus mediated disease; pharyngitis; tonsillitis; scarlet fever; sepsis; erysipelas; fasciitis; pneumonia; acute rheumatic fever; poststreptococcal glomerulonephritis; cellulitis; bacteraemia; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 AISTROYNWINILPTYSGRESNVORMAISELMADVGISVDMDYGPSSGSAGSSRVORALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTQSKYLMIYKDNETLDSNTQIEVYLTT - - - KQPVVKSLLDSKGIHYNQGNPYNLLTPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. pyogenes cysteine protease speB7 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVNWGWGGVSDGFFRLDALNPSALGTGGGGGGFNGYQSAVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.1%; Score 1327.5; DB 91.5%; Pred. No. 2.2e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                        Disclosure; Page 12; 97pp; English.
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                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE
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                95WO-US011723
                                                    94US-00306542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Simitarity .... Matches 258; Conservative
                                                                                                                           Kapur V;
                                                                                                                                                          1996-179944/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 398 AA;
                                                                                                                                                                           N-PSDB; AAT15294
                                                  14-SEP-1994;
                13-SEP-1995;
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                                                                                                                           Musser JA,
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Length 248;

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Disclosure; Page 59-61; 99pp; English
                                                         Matches 248; Conservative
                                              Similarity
              Sequence 248 AA;
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Misc-difference
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                                    Query Match
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                                                                                                                QPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHN 280
                                                                                                                                                                         61 YPNKGLKDYTYTLSSNNPYFNIPKNLFAAISTRQYNWANILPTYSGRESNVQKMAISELM 120
                                                                                                                                                                                                                        ADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQN 180
                                                                                                                                                                                                                                                                    YPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELM 340
                                                                                                                                                                                                        ADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQN 400
                                                                                                                                                                                                                                                       OPVYYOGGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFN 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or I cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes mature pyrogenic exotoxin B (SpeB) protein. This sequence is used in the invention
                                                                                                                                      9
SPEb). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence represents the wild-type SPEb mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superantigen toxin; vaccine; infection; pyrogenic exotoxin B; SpeB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes mature pyrogenic exotoxin B (SpeB) protein.
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0
                                                                   Length 248;
                                                                   Match 53.3%; Score 1332; DB 7; Length 2 Local Similarity 100.0%; Pred. No. 4.7e-100; es 248; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 AAE37686 standard; protein; 248 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-2001; 2001WO-US046540
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                         241 GYQSAVVG 248
                                                                                                                                                                                                                                                                                                    GYOSAVVG 468
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                                               Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003056015-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                06-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ulrich RG;
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                                                                   Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                        400
                                                                                                                                                                                                                                                                                                                                                                         121 ADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 QPVYYQGGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFN 240
                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pre-pro; cysteine; protease; inhibition; neoplastic; proliferation; cel. human; treatment; carcinoma; sarcoma; melanoma; lymphoma; leukaemia; leukemia; blood; lung; mammary gland; prostate; intestine; stomach; liver; heart; skin; pancreas; brain tissue; wound covering; prevention; metastasis; identification; speB7.
                                                                                                                            QPVVKSLLDSKG1HYNQGNPYNLLTPV1EKVKPGEQSFVGQHAATGCVATATAQ1MKYHN
                                                                                                                                                                             1 OPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHN
                                                                                                                                                                                                                                  281 YPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELM
                                                                                                                                                                                                                                                                                                                                           ADVGI SVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQN
                                                                       Gaps
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                                                                          Indels
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                   Score 1332; DB 7; I
Pred. No. 4.7e-100;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333. .338
/label= nucleotide_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "corresponding codon TAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ananthaswamy H,
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53.3%; Scc.
100.0%; Pred
0; M
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(TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYOSAVVG 248
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N-PSDB; AAT45219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes mature mutant pyrogenic exotoxin A (SpeA)-mature mutant SpeB fusion protein. This sequence is used in the invention. Note: This sequence is not shown in the specification, but is derived from S. pyogenes mature wild-type SpeA-SpeB protein (AAE37684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MOODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                    Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA; gene therapy; fusion protein; SpeB; mutant; mutein.

    S. pyogenes mature mutant SpeA-mature mutant SpeB fusion protein.

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                                                                                                                                                                                                                                                                                                       /note= "Wild type Cys substituted with Ser"
                                                                                                                                                                                                                                                                            'note= "Wild type Leu substituted with Arg"
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0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
                                                                                                                                                                                                                                                   note= "Encoded by GCT"
                                                                                                                                                                                                                        Location/Qualifiers
                        AAE37691 standard; protein; 468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 14; Page; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-2001; 2001US-00002784
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.6
Matches 466; Conservative
                                                                                                                                                                              Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-492125/46.
                                                                                                                                                                                                                                                                                          Misc-difference 267
                                                                                                                                                                                                                                                               Misc-difference 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 468 AA;
                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                    WO2003056015-A1
                                                                               06-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ulrich RG;
                                                                                                                                                                                           Synthetic
                                                   AAE37691;
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RESULT 3
            AAE3769
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fragment is altered so that binding of the encoded altered toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHZ class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-I (toxic shock syndrome toxin) superantigen toxin, peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, an treating/ameliorating a superantigen-associated bacterial infection, treating/ameliorating a superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-I superantigen toxin and an antibody which recognises altered TSST-I superantigen toxin and an antibody which recognises altered TSST-I. Also disclosed are mutated staphylococcal enterotoxin a and b (SPEa and SEE) SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
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                                                                                                                                                                                                                                                                 420
                                                                                                                                                                                                                                                                                        361 SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQNQPVYYQGGKVGGHAFVIDGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxin; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
                         181 SFWFDFFFPEPEFTQSKYLMIYKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
                                                                                 YNLLTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYF
                                                                                                            241 YNLITPVIEKVKPGEQSFVGQHAATGSVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYF
                                                                                                                                                                                                    10 NHPKNLFAAISTRQYNWNNILPTYSGRESNVQKWAISELMADVGISVDMDYGFSSGSAGS
                                                                                                                                                                         NHPKNLFAAISTROYNWNNILPTYSGRESNVOKMAISELMADVGISVDMDYGPSSGSAGS
                                                                                                                                                                                                                                                            SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQNQPVYYQGGKVGGHAFVIDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyrogenic enterotoxin a; vaccine; superantigen toxi superantigen-associated bacterial infection; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                           468
                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyrogenic toxin b, wild-type mature sequence.
                                                                                                                                                                                                                                                                                                                                                      DGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU62333 standard; protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00882431.
98US-00144776.
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exotoxin A;

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superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                       Superantigen toxin; vaccine; infection; pyrogenic gene therapy; fusion protein; SpeB.
                                                                                                                                                                                                                                                                                                                                              (USME-) US MEDICAL RES INST INFECTIOUS DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 134; 141pp; English.
                                                                                                                                                                                                                                            26-NOV-2001; 2001WO-US046540.
                                                                                                                                                                                                                                                                                          26-NOV-2001; 2001US-00002784
                                                                                                  Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-492125/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD56778.
                                                                                                                                            WO2003056015-A1.
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                                                                                                                                                                                                                                                                                                                                                                                          Ulrich RG;
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                                    The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) unfection, a vaccine (comprising an altered superantigen toxin for producing antigenist superantigen associated bacterial infection), treating/amellorating a superantigen-associated bacterial infection), treating/amellorating a superantigen-associated bacterial infection), creating/amellorating a superantigen-associated bacterial infection), an antisera isolated from individuals immuniated with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1 Superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB, SEC1) and streptococcal pyrogenic enterotoxin A, B, C1 (SEA, SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SFB, and Composition for treating or preventing bacterial infection. The present sequence represents the SPEB ILAZR/SPEB (478 mutant fusion protein. Note: The present sequence is described as having the Cys to Ser mutation in the SPEB portion at residue 257 (corresponding to amino acid 47 of mature composition for treating and security and security and security and security and security and security and security and security and security and security and security and security and security and security and security and security and security and security and security and security as a security and security and security and security and security as security and security and security and security and security and security and security and security and security and security and security and securit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOODPDPSQLHRSSLVKNLONIYFLYEGDPVTHENVKSVDOLRSHDLIYNVSGPNYDKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 2500; DB 7;
; Pred. No. 6.9e-195;
0; Mismatches 0;
Page 44-46; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPEb), but the residue is still Cys
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100.0%;
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Best Local Similarity 100.
Matches 468; Conservative
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Claim 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VSIDGIQSLSFDIETNKKAVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSQNQPVYYQGGKVGGHAFVIDGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                       9
The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin A (SpeA)-SpeB fusion protein. This sequence is used i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFWFDFFPEPEFTOSKYLMIYKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 YNLJTPVIEKVKPGEQSFVGQHAATGCVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYF
                                                                                                                                                                                                                                                                                                                                                                                              TELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSACIGGYTNREGNHLEIPKKIVVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFWFDFFPEPEFTQSKYLMIYKDNETLDSNTQIEVYLTTKQPVVKSLLDSKGIHYNQGNP
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                                                                                                                                                                                                                                                                      Length 468;
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                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                    100.0%; Score 2500; DB 7;
100.0%; Pred. No. 6.9e-195;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                           Sequence 468 AA;
                                                                                                                                                                          the invention
                                                                                                                                                                                                                                                                                                                       Matches 468;
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Streptococcus pyogenes SpeA-SpeB fusion protein.

(first entry)

06-OCT-2003

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Aar13209 Abr/62017 Abb/62017 Aaw121097 Aaw12146 Aaw12145 Aaw12147 Aaw12147 Aaw12147 Aaw12147 Aaw12149 Aaw12153 Aaw12153 Aaw12153 Aaw12159 Aaw12159 Aaw12159 Aaw12159 Aaw12169 Aaw12169 Aaw12169 Aaw12169 Aaw12169 Aaw12169

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New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
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Misc-difference 100. 101

Misc-difference 111. 212

Misc-difference 386. 387

Misc-difference 386. 387

Misc-difference 386. 387
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/note= "Encoded by GGTGTCGGT"
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                                                                                  AAR45017
ABB76240
AAW12097
AAW2097
AAW2164
AAW12164
AAW12145
AAW12140
AAW12140
AAW12150
AAW12
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98US-00144776.
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WPI; 2003-492125/46.
N-PSDB; ACD28908.
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01-SEP-1998;
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Aaw07898 Streptoco
Aar958856 S. pyogen
Aa481812 S. pyogen
Abu62332 Streptoco
Aba57685 Streptoco
Aae37690 S. pyogen
Aae37690 S. pyogen
Aab37699 Streptoco
Aae37689 S. pyogen
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Aae37691 S. pyogen
Abu62333 Streptoco
Aae37686 Streptoco
                                                                                                                                                                                             September 17, 2005, 00:47:53; Search time 152.962 Seconds (without alignments) 1183.322 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                            US-10-002-784A-27
2500
1 MQQDPDPSQLHRSSLVKNLQ......ALGTGGGAGGFNGYQSAVVG 468
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      OM protein - protein search, using sw model
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AAW07898
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ABU62332
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AAE37688
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ADR83971
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Gapop 10.0 , Gapext 0.5
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geneseqp2008:*
geneseqp2001s:*
geneseqp2003as:*
geneseqp2003as:*
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geneseqp1980s:*
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No.
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CORRESPONDENCE ADDRESS:
ADDRESSER: Charles H. Harris
STREET: US Army MRWC -504 Scott Street MCWR-JA (Charles H. Harris-
CITY: FORT DETRICK
STATE: MARYLAND
COUNTY: USA
ZIP: 21702-5012
COMPUTER: READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: Apple Macintosh 7.5
SOFTWARE: Miscintosh 7.5
SOFTWARE: June 25, 1997
CLASSIFICATION UNWBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION UNWBER: 34,616
FILING DATE: APPLICATION:
NAWE: Charles H. Harris
REGISTRATION NUMBER: 34,616
REGISTRATION NUMBER: 34,616
REGISTRATION INFORMATION:
NAWE: Charles H. Harris
TELECOMMUNICATION INFORMATION:
TELEPONE: (301) 619-2065
TELEPAX: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 LRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA---- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 ----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 VRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNET 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 TRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFAQSKYLMMYNDNKM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 VLVTFLGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ 70
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42.9%; Score 567.5; DB 4; Length 266;
Best Local Similarity 47.5%; Pred. No. 1.8e-46;
Matches 121; Conservative 40; Mismatches 75; Indels 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 vĎSKDVKIĖVYĽTTK 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-882-431B-6
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                                                                                                                                                                                                                                                           Sequence 8, Application US/09414276
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION;
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Arntzen, Charles
; TITLE OF INVENTION: Genini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APLICATION NUMBER: US/09/414,276
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SAINVKSIDQSLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YFSKKTNDINSHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKK 180
                        183 YLVKNKKLYEPUNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDGSKYLMMYNDNKMVDS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KVTAOELDYLTRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDOSK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 THENVKSVDQLRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 YLCENA-----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 MVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSK 226
--ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LKKMVFF---VLVTFLGLTIS-QEVFA--QODPDPSQLHRSSLVKNL-QNIYFLYEGDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

43.5%; Score 575; DB 3;
Best Local Similarity 47.2%; Pred. No. 3.5e-47;
Matches 125; Conservative 40; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Bacterial Superantigen Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 YLMMYNDNKMYDSKDVKIEVYLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 YLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: bean yellow dwarf virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS
                                                                                                                                                       240 NTSQIEVYLTTK 251
                                                                                                                                                                                           242 KDVKIEVYLTTK 253
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LENGTH: 266
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71 LRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA---- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 ----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 VRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNET 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 TRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFAQSKYLMMYNDNKM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 VLVTFLGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
ADDRESSEE: Charles H. Harris
STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.9%; Score 567.5; DB 3; Best Local Similarity 47.5%; Pred. No. 1.8e-46; Matches 121; Conservative 40; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
FLING DATE: 01-Sep-1998
PRICASIFICATION: <Unknown>
PRICATICATION DATA:
APPLICATION NUMBER: 08/882,431
                                                                                                                                                                                                                                   COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: «UI
TELECOMMUNICATION: 1010 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08882431B Patent No. 6713284
                                                                                                                                                            ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
                                                                                          CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 LDSNTSQIEVYLTTK 251
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182 YLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFPPEP--EFTQSKYLMIYKDNETLDS 239
                                                                                                                                                                                                                                                                       183 YLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKAVDS 241
                                                                                   74 HDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA----- 123
                                                                                                                                                                  124 -- ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 VLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQLRS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 VLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYBGDPVTHENVKSVDQLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 HDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Blmslie, Robyn B.
APPLICANT: Elmslie, Robyn B.
APPLICANT: Bcter. Terence A.
IITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READALE FORM:
MEDIUM TERE FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2879-29-C1
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Patent No. 5935568
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J
REGISTRATION NUMBER: 32,020
REFRENCE/DOCKET NUMBER: 2879
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 255 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                               240 NTSQIEVYLTTK 251
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242 KDVKIEVYLTIK 253
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LENGTH: 255 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-580-806-2
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                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-08-580-806-2
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                  64 NQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACLYGGVTNHEGNHLEIPKKIVVKVSI 123
                                                                                                                                                                                                                                                                                                                                                                                                                               94 NOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSI 153
                                                                                                                                                                                                                                                                                                                                                                                                          DGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 213
                                                                                                                                                                                                                                                                                 4 PKPSQLQRSNLVKTFKIYIFFMRVTLVTHENVKSVDQLLSHDLIYNVSGPNYDKLKTELK 63
                                                                                                                                                                                                                                              34 PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKTELK
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                  Length 220;
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                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
                                                                                                                                                                                                        24;
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44.5%; Score 588; DB 1; Lo
Best Local Similarity 47.2%; Pred. No. 1.9e-48;
Matches 119; Conservative 41; Mismatches 76;
                                                                                                                                                                  DB 4;
                                                                                                                                                              Score 979.5; DB 4
Pred. No. 3.7e-86;
4; Mismatches 24
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NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
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NAME: Kovarik, Joseph E.
REGISTATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-023
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                             TYPE: PRT
ORGANISM: Streptococcus pyogenes
                                                                                                                                                                74.1%;
86.7%;
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amino acid
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Best Local Similarity 86.74
Matches 189; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1700 Linc
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                       US-09-708-008B-20
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                                       SEQ ID NO 20
LENGTH: 220
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TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE FILE REFERENCE: 600.311USWO
CURRENY PAPLICATION NUMBER: 1999-03.391C
CURRENY FILING DATE: 1999-03.12
PRIOR APPLICATION NUMBER: PCT/US96/10252
PRIOR PILING DATE: 1996-06-07
PRIOR PILING DATE: 1996-06-07
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 14
LENGTH: 221
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Pred. No. 8.7e-104;
0; Mismatches 2; Indels
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TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOKINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS;
FILE REPERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
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Pred. No. 3.7e-86;
4; Mismatches 24
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; Sequence 20, Application US/08896933
? Eatent No. 6221351
; GENERAL INFORMATION:
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US-08-896-933-20
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86.7%;
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Best Local Similarity 99.1%;
Matches 219; Conservative
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Best Local Similarity 86.7
Matches 189; Conservative
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94 NQEMATLEKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSI 153
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Pred. No. 3.7e-86;
4; Mismatches 24; Indels 1.
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; Batent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR FILING DATE: 1997-07-18
; PRIOR FILING DATE: 1994-06-02
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GERNEAL INFUGNATION:

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

TITLE OF INVENTION: SUPERANTICENS, AND RELATED COMPOUNDS;

FILE REPERSORS: 05629/00504

CURRENT APPLICATION NUMBER: US/09/314,235

CURRENT PILING DATE: 1999-0-5-18

EARLIER APPLICATION NUMBER: 08/896,933

EARLIER FILING DATE: 1997-07-18

EARLIER FILING DATE: 1997-07-18

EARLIER FILING DATE: 1997-0-0-18

EARLIER FILING DATE: 1991-01-17

EARLIER PILING DATE: 1991-01-17

EARLIER FILING DATE: 1991-01-17

EARLIER FILING DATE: 1990-01-17

EARLIER FILING DATE: 1990-10-03

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 20

EARLIER FALENG DATE: 1990-10-03

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 20

EARLIER FALENG DATE: 1990-10-03

EARLIER FILING DATE: 1990-10-03
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                               183 FDFFPEPEFTGSKYLMIYKONETLDSNISQIEVYLTTK 220
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86.7%;
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Best Local Similarity 86.77
Matches 189; Conservative
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US-09-708-008B-20
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214
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99.1%; Pred. No. 7e-104;
tive 0; Mismatches 2; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
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US-08-973-391C-14
Sequence 14, Application US/08973391C
Sequence 14, Application US/08973391C
GENERAL INFORMATION:
APPLICANT: SCAllaevert, Patrick M.
APPLICANT: Stocht, Jennifer
APPLICANT: Ohlendorf, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Streptococcus pyogenes US-09-708-008B-29
                              219; Conservative
  Best Local Similarity
Matches 219; Conserv
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US-09-708-008B-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.0%; Score 1164; DB 3; Length 221; 99.1%; Pred. No. 7e-104;
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CANDELL INFORMATION:
CANDELL INFORMATION:
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTGENS, AND RELATED COMPOUNDS;
FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER FILING DATE: 1999-05-18
EARLIER FILING DATE: 1994-06-02
EARLIER FILING DATE: 1994-06-02
EARLIER FILING DATE: 1994-06-01
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1991-01-17
EARLIER FILING DATE: 1990-01-17
EARLIER FILING DATE: 1990-00-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                   APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS, TITLE OF INVENTION: SUPERANTICENS, AND RELATED COMPOUNDS FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER PILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEWEDFFPEPEFTQSKYLMIYKDNETLDSNTSQIEVYLTTK 251
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5-08-896-933-29
Sequence 29, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
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Patent No. 6338845
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.1'
Matches 219; Conservative
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LENGTH: 221
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LENGTH: 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/09708008B

Patent No. 669746

GENERAL INFORMATION:
APPLICAMT TERMAN. David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUBERANTIGENS, AND RELATED COMPOUNDS;
FILE REFERENCE: 09629/005002;
CURRENT APPLICATION NUMBER: US/09/708,008B

CURRENT FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: US/08/896,933

PRIOR FILING DATE: 1997-07-18

PRIOR PLICING DATE: 1994-06-02

PRIOR FILING DATE: 1994-06-02
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Sequence 13, Application US/08973391C

Sequence 13, Application US/08973391C

Retent No. 6632441

GENERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
APPLICANT: Schlievert, Pannela
APPLICANT: Schoen, Jennifer
APPLICANT: Scener, Jennifer
APPLICANT: Ollendorf, Douglas
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
FILE REFERENCE: 600.3110SMO
CURRENT APPLICATION NUMBER: US/08/973,391C
CURRENT APPLICATION NUMBER: US/08/973,391C

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

SOFTWARE: Patentin version 3.1
                                                                                                                             61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                          ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
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                                            1 MENNKKYLKKWYFFVLVTFLGLTISQEVFAQQDPDFSQLHRSSLVKNLQNIYFLYEGDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Streptococcus pyogenes
US-08-973-391C-13
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Patent No. 6713284

GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SCUURNCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MEMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: PORT DETRICK
STREET: WARVLAND
COUNTRY: USA
                                                                                                                                                                          61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                                                                                           121 ENAERSACIYGGYTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
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                                                                                                                                                 61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                                                                    ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
                                                                                                                                                                                                                                                                                                                       KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPFFTQSKYLMIYKDNETLDSN 240
                                                                                  1 MENNKKVLKKOWVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV 60
                                                            1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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1 Similarity 100.0%; Pred. No. 5.6e-119; 251; Conservative 0; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: JUNEAR 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 619-2065
TELEPAX: (301) 619-714
INPORMATION FOR SEQ ID NO: 16;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          241 TSQIEVYLTTK 251
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STRANDEDNESS: Unl
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US-08-882-431B-16
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27, Appl 27, Appl 27, Appl 21, Appl 21, Appl 24, Appl 24, Appl 25, Appl 25, Appl 112, Appl 112, Appl 112, Appl 112, Appl 112, Appl

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

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Length 251;
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ADDRESSEE: Charles H. Harris
STREET: US ARMY MRMC -504 Scott Street
MCMR.JA (Charles H. Harris-Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
US-08-896-933-27
US-09-314-235-27
US-09-314-235-27
US-09-314-235-21
US-09-708-008B-21
US-09-708-008B-21
US-09-714-708B-24
US-08-882-431B-24
US-09-314-235-25
US-09-314-235-25
US-09-314-235-25
US-09-314-235-25
US-08-486-099-112
US-08-484-223B-112
US-08-919-597-112
US-08-919-597-112
US-08-919-597-112
US-08-919-597-112
US-08-919-597-112
US-08-919-597-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
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MEDIUM TYPE: Bloppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: 40hknown>
                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1322;
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MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
18-09-144-776B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/09144776B Patent No. 6399332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
STRANDEDNESS: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
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 LENGTH: 251
                 US-09-144-776B-16
   Query Match
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                                                                                                                          September 17, 2005, 00:42:17; Search time 13.9638 Seconds (without alignments) 1341.817 Million cell updates/sec
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1 MENNKKVLKKMVPFVLVTFL......KDNETLDSNTSQIEVXLTTK 251
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-144-776B-8
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                                                                                                                                                                                                                                                              Query Match
41.7%; Score 551.5; DB 1; Length 266;
Best Local Similarity 46.1%; Pred. No. 3.2e-33;
Matches 117; Conservative 46; Mismatches 74; Indels 17; Gaps
                                                                                                                                                                                                                                                  30671 MW; SED8A32D11FFCA59 CRC64;
 Enterotoxin type C-3.
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    129 GKVTGGKTCMYGGITKHEGNHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDI 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ER----SACIYGGVTNHEGNHLEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDY 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 MVF-FVLVTFLGLTISQEVFAQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hizamateu K.; "Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.8%; Score 553; DB 2; Length 266; 44.5%; Pred. No. 2.5e-33; Live 51; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 AA; 30670 MW; 4C654659AA48120F CRC64;
                                                                                                                              Last annotation update)
                                                                                                                                                                                      Staphylococcus aureus (strain MM2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
                                                                                                        sequence update)
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01-NOV-1991 (Rel. 20, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
ELECTCOXIN type C-3 precursor (SEC3).
Name=entC3; OrderedLocusNames=SAV2009, SA1817;
                                             266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP004824; BAB94624.1; -...
HSSP; P34071; 1STE.
GO: GO: GOOS576; C: extracellular; IEA.
GO: GO: MO09405; P: pathogenesis; IEA.
InterPro; IPR008992; Bact endoctox.
InterPro; IPR008992; Bact endoctox.
InterPro; IPR006123; Stap/Strept tox.
InterPro; IPR006123; Stap/Strept tox.
InterPro; IPR006126; Stap/Strept tox.
Pfam; PF021876; Stap_Strp_Coxin.
Pfam; PF021876; Stap_Strp_Coxin.
PROSITE; PS00279; BACTRITOXIN.
PROSITE; PS00279; BACTRITOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN.1; PROSITE; PS00279; STAPH_STREP_TOXIN.2; 1.
                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last seq.
01-OCT-2003 (TrEMBLrel. 25, Last annc
ENTENCYOXIN TYPE C.
Name=sec4; OrderedLocusNames=WW0759;
                                         PRT;
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les 114; Conservative
                                         PRELIMINARY;
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SEQUENCE 266 AA;
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P23313;
01-NOV-1991
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                                                                                                                                                                                                                                            STRAIN=MUSO / ATCC 700699, and N315;
STRAIN=MUSO / ATCC 700699, and N315;
STRAIN=MUSO / ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Marsumaru H., Maruyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hovde C.J., Hackett S.P., Bohach G.A., "Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison of all three type C staphylococcal enterotoxins."; Mol. Gen. Genet. 220:329-313(1990).
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-1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases
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InterPro; IPR006992; Bact endotox.
InterPro; IPR00617; Bctr1 tox.
InterPro; IPR006126; Staph/Strept toxin.
InterPro; IPR006126; Staph/Strept tox.
InterPro; IPR006173; Staph tox OB.
Pfam; PF01123; Stap Strp_tox Cox C; I.
PR07175; PR00279; BACTRITOXIN.
PR087175; P800279; BACTRITOXIN.
PR087175; P800279; STAPH STREPT TOXIN 1; 1.
BR087176; SG0278; STAPH STREPT TOXIN 2; 1.
3D-structure; Complete Proteome; Enterotoxin; Signal; Superantigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97064178; Pubmed-8906797; DOI=10.1038/384188a0; Fields B.A., Malchiodi E.L., Li H., Ysern K., Stauffacher C.V., Schlievert P.M., Karjalainen K., Mariuzza R.A.; "Crystal structure of a T-cell receptor beta-chain complexed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
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Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain N315), and
                                                                                                                    Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=158878, 158879, 1280;
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PDB; 1JVMM; X-ray; D=28-266.
PDB; 1JVMS; X-ray; D=28-266.
PDB; 1JVMJ; X-ray; D=28-266.
PDB; 1KLG; X-ray; D=28-266.
PDB; 1KLU; X-ray; D=28-266.
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                                            Staphylococcus aureus Staphylococcus aureus.
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SHQTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 DKFLAHDLIYNISDKKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ER----SACIYGGVTNHEGNHLEIPK--KIVVKVSIDGIQSLSFDIETNKKMVTAQELDY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVRKYLTDUKQLYTNGPSKYETGYIKFIPROKESFWFDFFPEP--EFTQSKYLMIYKDNE 235
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SEQUENCE FROM N.A.
MEDLINE=20566668; PubMed=11114901; DOI=10.1128/JB.183.1.63-70.2001;
Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
Meaney W.J., Smyth C.J.;
"Characterization of a putative pathogenicity island from bovine
Staphylococcus aureus encoding multiple superantigens.";
J. Bacteriol. 183:63-70(2001).
EMBL: AF217235; AAG225599.1;
HSSP: P34771; 114X.
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                                                                                        11 MVF-FVLVTFLGLTISQEVFAQODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSV
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GO; GO:00055/6; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR006177; Btap/Strep_toxin.
InterPro; IPR006173; Stap/Strep_toxin.
InterPro; IPR006123; Stap/Strep_toxin.
InterPro; IPR006124; Stap/Strep_toxin.
InterPro; IPR006125; Stap/Strp_toxin.
InterPro; IPR006125; Stap/Strp_toxin.
IPEAM; PF01223; Stap_Strp_tox.C; 1.
IPEAM; PF02876; Stap_Strp_tox.C; 1.
IPEAM; PR02779; BACTRLTOXIN.
IPROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.
IPROSITE; PS00277; STAPH_STREP_TOXIN 2; 1.
IPROSITE; PS00277; STAPH_STREP_TOXIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 42.0%; Score 555; DB 2; Length 27. Local Similarity 44.9%; Pred. No. 1.8e-33; nes 115; Conservative 51; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Staphylococcal enterotoxin C-bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus
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TVDSKSVKIEVHLTTK 269
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VDSKDVKIEVYLTTK 264
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                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                               Name=sec-bov;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 VLVTFLGLTIS-QEVFA--QODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ
                                                                                                                                                                                                                                                                         DDN -> NND (in Ref. 3).
DQPLYFDLI -> NBFFDLIYL (in Ref. 3).
Missing (in Ref. 3).
DIN -> NID (in Ref. 3).
QTD -> ENT (in Ref. 3).
NG -> GN (in Ref. 3).
Y -> YY (in Ref. 3).
QE -> EQ (in Ref. 3).
D -> N (in Ref. 3).
D -> N (in Ref. 3).
               InterPro; IPRO06125; Staph/Strept_tox.
InterPro; IPR006173; Staph.tox OB.
Pfam; PF012876; Stap_Strp_tox_C; 1.
Pfam; PF012875; Stap_Strp_tox_T; 1.
PRINTS; PR00279; BACTRITOXIN.
PROSITE; PS00279; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
3D-Structure; Direct protein sequencing; Enterotoxin; Signal; Superantigen; Toxin.
1 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31436 MW; B6D417F61CF018B0 CRC64;
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      InterPro; IPR006123; Stap/Strep_toxin.
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266 AA;
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MEDLINE=85298255; PubMed=3898073;
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                                                               WEDLINE=9913798; PubMed=9952369;
WA MEDLINGE=9913798; PubMed=9952369;
WA PEDLINGE=9913798; PubMed=9952369;
WA HOLLINGEAG S.K., Beall B.;
A HOLLINGAGE S.K., Beall B.;
Tropism in group A streptococci.";
Tropism in group A streptococci.";
Tropism in group A streptococci.";
WEMBL, AF029051; AAD21315.1;
WEMBL, AF029051; AAD21315.1;
WEMBL, AF029051; Stab AD21315.1;
WEMBL, AF029051; Stab AD21315.1;
WEMBL, AF029051; Stab AD21315.1;
WEMBL, AF029051; Stab AD21315.1;
WEMBL, AF029051; Stap Stropt coxin.
WENTERPRO; IPR006123; Stap Stropt coxin.
WENTERPRO; IPR006123; Stap Stropt coxin.
WENTERPRO; IPR006123; Stap Stropt coxin.
WENTERPRO; IPR006124; Stap Stropt coxin.
WENTERPRO; IPR006175; Stap Stropt coxin.
WENTERPRO; IPR006175; Stap Stropt coxin.
WENTERPRO; IPR006175; Stap Stropt coxin.
WENTERPRO; PR008176; STAP STREP TOXIN. 1; 1.
WENSITE; PS00277; STAPH STREP TOXIN. 2; 1.
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MEDLINE-86168029.
Jones C.L., Khan S.A.,
"Nucleotide sequence of the enterotoxin B gene from Staphylococcus
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                    79.7%; Score 1054; DB 2; Length 222; 89.2%; Pred. No. 8.4e-71;
                                                                                                                                                                                                                                                                                                                                        Indels
Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 YIKFISKDKETFWFDFFPEPEFFNQVKYLMIYKDNETLDSSTS 222
                                                                                                                                                                                                                                                                                                25884 MW; 121F8460992818F8 CRC64;
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 AA
                                                                                                                                                                                                                                                                                                                                       12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last seq
25-OCT-2004 (Rel. 45, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 166:29-33(1986).
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SEQUENCE OF 40-91 FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                 222 AA;
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Matches 198; Conserv
                                                 SEQUENCE FROM N.A.
                             NCBI_TaxID=1314;
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SEQÜENCE
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Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
Molecular cloning of staphylococcal enterotoxin B gene in Escherichia
coli and Staphylococcus auvens.";
Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
                                                                                                                                                                                                                                               Huang I.-Y., Bergdoll M.S.; "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence."; J. Biol. Chem. 245:3518-3525(1970).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94203282; PubMed=8152483; DOI=10.1038/368711a0;
MEDLINE=94203282; PubMed=8152483; DOI=10.1038/368711a0;
Jardetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
Chi Y.I., Stauffacher C., Strominger J.L., Wiley D.C.;
"Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen.";
Nature 368:711-718(1994).
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beta chain and the superantigen staphylococcal enterotoxin B.";
Immunity 9:807-816(1998).
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PDB, 1SBB; X-ray; B/D=28-266.
PDB, 1SB3, X-ray; B/D=28-266.
PDB, 1SB4; X-ray; 0=28-266.
PDB, 1SBB; X-ray; 0=28-266.
PDB, 1SBB; X-ray; D/H=29-262.
PDB, 1SBB; X-ray; 0=28-266.
INTERPO: 1PR008992, Bact endotox.
INTERPO: 1PR008992, Bact endotox.
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1D5X; X-ray; C=28-266.
1D5Z; X-ray; C=28-266.
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LYTNGPSKYETGYIKFIPKNKESFWFDFFPEFFTQSKYLMIYKDNETLDSNTSQI
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pyrogenic exotoxin A (Fragment).
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89.2%; Pred. No. 8.4e-71;
ative 12; Mismatches 12;
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MEDLINE=22508029; PubMed=12620634;
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01-MAY-2000 (TEMBLrel. 13,
01-MAY-2000 (TEMBLrel. 13,
01-OCT-2003 (TEMBLrel. 25,
Exotoxin_type A (Fragment).
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NCBI_TaxID=119602;
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MELINE=92044323; PubMed=1940804;

MEDLINE=92044323; PubMed=1940804;

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MELINE=92044323; PubMed=1940804;

MELINE=92044323; PubMed=1940804;

The station and clonal distribution of four alleles of the gene encoding pyrogenic exotoxin A (scarlet fever toxin) in gene encoding pyrogenes.";

The station and clonal distribution of four alleles of the gene encoding pyrogenes.";

J. Exp. Med. 174:127-11274(1991).

EMBL; X61573; CAA43771.1;

MENSP; PO1552; CEXTRACELULAR; IEA.

GO, GO:0005576; C:extracellular; IEA.

GO, GO:0005576; C:extracellular; IEA.

GO, GO:0005576; C:extracellular; IEA.

MRSP; PRO06575; B:pathogenesis; IEA.

InterPro; IPR006123; Stap/Strept.tox.

InterPro; IPR006123; Stap/Strept.tox.

InterPro; IPR006123; Stap/Strept.tox.

InterPro; IPR006124; Stap/Strept.tox.

PR Pfam; PR0123; Stap_Strp_tox.

PRINTS; PR00277; STAPH_STREP_TOXIN_1; 1.

PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
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83.9%; Score 1109; DB 2; Length 2
Best Local Similarity 88.6%; Pred. No. 7.1e-75;
Matches 209; Conservative 14; Mismatches 13; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
Hollingshead S.K., Bealol B.;
Hollingshead S.K., Bealol B.;
Genetic linkage of exclosin alleles and emm gene markers for tissue tropism in group A streptococci.";
J. Infect. Dis. 179:627-636(1999).
EMBL, AF055698; AA01089.
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Last annotation update)
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93.3%; Score 1234; DB 2;
Best Local Similarity 99.2%; Pred. No. 3.4e-84;
Matches 234; Conservative 0; Mismatches 2;
                                                                                                                                                                                        type A exotoxin.
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:000576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR006177; Bctrl_tox.
InterPro; IPR006128; Stap/Strept_toxin.
InterPro; IPR006128; Staph/Strept_toxin.
InterPro; IPR006128; Staph/Strept_toxin.
InterPro; IPR006128; Staph/Strept_toxin.
InterPro; IPR006173; Staph tox OB.
Pfam; PF01123; Stap_Strp_toxin; I.
Pfam; PR01123; Stap_Strp_toxin; I.
PRNNTS; PR00279; BACTRITOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; I.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; I.
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InterPro; IPR006173; Staph tox OB.
Pfam; PF01123; Stap_Strp_toxin; 1.
Pfam; PF02876; Stap_Strp_tox C; 1.
PRINTS; PR00277; STAPH STREP TOXIN 1; 1.
PROSITE; PS00277; STAPH—STREP_TOXIN 1; 1.
                                                                                                                                                                   Potential.
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23 >2
236 2
236 AA;
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Best Local Similarity
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NCBI_TaxID=1314;
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A Melson K., Schlevert P.M., Selander R.K., Musser J.M.;

T characterization and clonal distribution of four alleles of the speak

T gene encoding pyrogenic exotoxin A (scarlet fever toxin) in

Streptococcus pyrogenes ";

J. Exp. Med. 174.1271-1274(1991).

B. Exp. Med. 174.1274(1991).

B. Exp. Med. 174.1274(1991
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                                                                                      Length 222;
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                                                                                                                                                                    1; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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25759 MW; 48BB7ADDCD91FBA3 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                             Query Match 88.7%; Score 1173; DB 2; Best Local Similarity 99.5%; Pred. No. 1.1e-79; Matches 221; Conservative 0; Mismatches 1;
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99.5%; Pred. No. 1.2e-78;
iive 0; Mismatches 1;
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type A exotoxin.
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STRAIN=MGAS500;
MEDLINE=92044323; PubMed=1940804;
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222 AA;
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68 9

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61 DQLLSHDLIYNVSGPNYDKLKTELKNOEMATLFKDKNIDIYGVEYYHLCYLCENAERSAC 120
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A MEDLIANES-ZOGATAZZJ, FUDMOGEL 194004;

T "Characterization and clonal distribution of four alleles of the concoling pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";

L J. Exp. Med. 174:1274.[1991).

E RMBL; X61562; CAA43760.1; -...

E RMBL; X61564; CAA43760.1; -...

R EMBL; X61564; CAA43762.1; -...

R EMBL; X61565; CAA43765.1; -...

R EMBL; X61567; CAA43765.1; -...

R PIR; A60108; A60108.

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005577; BCTL tox.

R InterPro; IPR006123; Stapl/Strept_toxin.

R InterPro; IPR006123; Stapl/Strept_tox.
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STRAIN=MGAS156, MGAS250, MGAS285, MGAS480, MGAS492,
                                                                                                                                                                                                                                                                                        Score 1239; DB 2; Length 236;
Pred. No. 1.4e-84;
1; Mismatches 1; Indels (
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23 >236 type A exotoxin.
236 AA, 27468 MW, 29DF2AD575623A84 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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InterPro; IPR006126; Staph/Strept_tox.
InterPro; IPR006173; Staph tox. OB.
Pfam; PF01123; Stap Strp toxin; 1.
Pfam; PF02876; Stap Strp_tox_C; 1.
PRNYS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH STREP_TOXIN 1; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.
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Name=speA;
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                                                                                                                                                                                                                                                                                          93.7%;
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Best Local Similarity 99.2<sup>3</sup>
Matches 234; Conservative
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C STRAIN-MCASS158, MCAS491, MCAS495, and MCAS624;

K MEDLINE-9204323; PubMed=1940804;

M MEDLINE-92044323; PubMed=1940804;

Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;

"Characterization and clonal distribution of four alleles of the gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogense.";

L J. Exp. Med. 174:1271-1274(1991).

R EMBL; X61569; CAA43766.1; -..

R EMBL; X61570; CAA43766.1; -..

R EMBL; X61571; CAA43769.1; -..

R EMBL; X61572; CAA43770.1; -..

R EMBL; X61572; CAA43770.1; -..
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23 >236 type A exotoxin.
236 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;
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Q1-NOV-1996 (TYEMBLrel. 01, Created)

01-NOV-1996 (TYEMBLrel. 01, Last sequence update)

05-JUL-2004 (TYEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        93.8%; Score 1240; DB 2;
99.6%; Pred. No. 1.2e-84;
tive 0; Mismatches 1;
               InterPro; IPR000992; Bact endotox.
InterPro; IPR006127; Bctr tox.
InterPro; IPR006123; Stap/Strept toxin.
InterPro; IPR006126; Stap/Strept toxin.
InterPro; IPR006127; Stap/Strept toxin.
InterPro; IPR006173; Stap toxin; 1.
Pfam; PF01123; Stap Strp toxin; 1.
PR081TE; PR00279; BACTR1TOXIN.
PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
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GO: GO:0009405; P:pathogenesis: IEA.
InterPro: IPR008992; Bact endotox.
InterPro: IPR006177; BctrI tox.
InterPro: IPR006123; Stap/Strep_toxin.
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    GO:0009405; P:pathogenesis; IEA
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Best Local Similarity 99.6
Matches 235; Conservative
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NCBI_TaxID=1314;
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Complete proteome. SEQUENCE 251 AA;
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Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
into phage evolution."
Genome Res. 13:1042-1055(203).
EMBL; AR014161; AAM799081; -.
EMBL; AP005142; BAC63655.1; -.
                                                                                                                                                                 1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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STRAIN-MGAS115 / Serotype M3;
MEDLINE-22131808; bubMed=12122206; DOI=10.1073/pnas.152298499;
MEDLINE-22131808; bubMed=12122206; DOI=10.1073/pnas.152298499;
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                  Query Match 99.5%; Score 1315; DB 1; Length 251; Best Local Similarity 99.6%; Pred. No. 3.3e-90; Matches 250; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                            29246 MW; 54001FE4CCCBFCC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Exotoxin type A-phage associated (SpeA precursor).
Name=speA3; OrderedLocusNames=SP80560, SpyM3_1301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         emergence.";
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
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251 AA;
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NCBI_TaxID=198466;
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X MEDLINE=92044323; PubMed=1940804;
A Nelban K., Schlievert P.M., Schladeder R.K., Musser J.M.;
A Nelban K., Schlievert P.M., Schladeder R.K., Musser J.M.;
I caracterization and clonal distribution of four alleles of the speat gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";
J J. Exp. Med. 174:1271-1274 (1991).
R EMBL; X61556; CAA43753.1; -..
R EMBL; X61559; CAA43753.1; -..
R EMBL; X61559; CAA43757.1; -..
R EMBL; X61559; CAA43758.1; -..
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1314; DB 2;
Pred. No. 3.9e-90;
HESP; POLSES; 1SEB.

GO; GO:0009576; C:extracellular; IEA.
GO; GO:0009505; P:pathogenesis; IEA.
InterPro; IPR008992; Bact endotox.
InterPro; IPR006127; BctrI_tox.
InterPro; IPR006127; BctrI_tox.
InterPro; IPR006126; Staph/Strept_toxin.
InterPro; IPR006126; Staph/Strept_toxin.
InterPro; IPR006126; Staph/Strept_toxin.
InterPro; IPR006126; Staph/Strept_toxin.
InterPro; IPR006126; Staph_tox_OB.
Pfam; PP01213; Stap_Strp_tox_C; I.
Pfam; PP02876; Stap_Strp_tox_C; I.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; I.
PROSITE; PS00278; STAPH_STREP_TOXIN_1; I.
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                    chain.
MISCELLANEOUS: This toxin seems to be coded by bacteriophage T12.
SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
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TNKGAVTAQELDYK -> QIKNGNCSRISYT (in Ref.
SUBUNIT: Binds to major histocompatibility complex class II beta
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SQEVPAQODDD -> LPKGICSTRPK (in Ref. H -> Q (in Ref. 2).
S -> N (in Ref. 2).
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InterPro; 1PR00617; Bctll tox.
InterPro; 1PR006123; Stap/Strep_toxin.
InterPro; 1PR006126; Staph/Strept tox.
InterPro; 1PR006126; Staph tox_OB_Fam: PP02876; Stap Strp_tox_OB_Fam: PP02876; Stap_Strp_toxin; 1.
PR01123; Stap_Strp_toxin; 1.
PR051TE; PS00279; BACTRLTOXIN.
PROSITE; PS00279; STAPH STREP_TOXIN_1; 1.
PROSITE; PS00279; STAPH STREP_TOXIN_1; 1.
3D-structure; Signal; Toxin.
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1FNU; X-ray; ...
1FNV; X-ray; ...
1FNW; X-ray; ...
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PUNCTION: Causative agent of the symptoms associated with scarlet
fever, have been associated with streptococcal toxic shock-like
disease and may play a role in the early events of rheumatic
                                                                                                                                                                                                           1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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                                                                                                                                        Gaps
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MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
O'Srien S.M., Tranter H.S., Acharya K.R.;
"Structural basis for the recognition of superantigen streptococcal pyrogenic exotoxin A (SpeAl) by MHC class II molecules and T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=86166804; PubMed=3514452;
Weeks C.R., Ferretti J.J.;
"Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86284313; PubMed=3526093;
Johnson L.P., L'Italien J.J., Schlievert P.M.;
"Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
related to Staphylococcus aureus enterotoxin B.";
Mol. Gen. Genet. 203:354-356(1986).
                                                                                                                                        .
                                                                                                     Query Match 99.5%; Score 1315; DB 1; Length 251; Best Local Similarity 99.6%; Pred. No. 3.3e-90; Matches 250; Conservative 0; Mismatches 1; Indels (
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                By similarity.
Exotoxin type A.
By similarity.
54001FE4CCCBFCC3 CRC64;
                                                                                                                    Pred. No. 3.3e
0; Mismatches
 Complete proteome, Signal, Toxin. SIGNAL 1 30 By 8
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                                                                    29246 MW;
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NCBI_TaxID=1314;
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1 MENNKKVLKKMVFFVLVTFL.....KDNETLDSNTSQIEVYLTTK 251
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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        Q6XZEF
        Q6XZEF
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        Q6XXEF
        Q6XZEF
        Q6XZEF
        Staphylococ

        37
        499
        37.7
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        Q6XMA
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        Q6XM3
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## ALIGNMENTS

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enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Jo.May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiab, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-258 «XUR»
A,Cross-references: UNIPROT:098ZM4; GB:BA000018; PID:g13701618; PIDN:BAB42911.1; GSPDB:
A,Experimental source: strain N315
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                                                                                                                                                               59 PVTHENVKSVDQLRSHDLIYN -- VSGPN - YDKLKTELKNQEMATLFKDKNVDIYGVEYYH 115
                                                                                                                                                                                                                                                            116 LCYLCENAE--RSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSL--SPDIETNKKMVT 171
                                                                                                                                                                                                                                                                                         172 AQELDYKVRKYLTDNKQLYT----NGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKY 227
                                                                                                                                                                                                                                                                                                                                                                                179 VQELDLQSRHYLHETYNLYNTDAFNG--KIQRGLIEFHPSSGDSVGYDLFG---AQGQY 232
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                               38; Gaps
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       34.1%; Pred. No. 1.2e-17; ative 52; Mismatches 86; Indels
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Job time : 19.153 secs
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                             91; Conservative
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C;Superfamily: enterotoxin B
Best Local Similarity
Matches 91; Conserv
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A;Molecule_type: DNA
A;Residues: 1-260 «KUR»
A;Cross-references: UNIPROT:099SU3; GB:BA000018; PID:g13701743; PIDN:BAB43036.1; GSPDB:
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C;Dete: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Dete: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A9969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shibb, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
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C;bate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C$9984
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
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                                                                                                                                        179 VRKYLTDNKOLYTNGPSKYETGYIKFIPKNKESFWFDFFPE--PEFTQSKYLMIYKDNET 236
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KANTRAGELDYKURKYLTDNKQLYTNGPSKYETGYIKF -- IPKNKESFWFDFFPEPEFTQS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146 A; Accession: A89969 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.5%; Score 337; DB 2; Length 136; 49.6%; Pred. No. 4.4e-18; ive 22; Mismatches 38; Indels
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                                                                                                                                                                                                                                 226 KYLMIYKDNETLDSNTSQIEVYLTT 250
                                                                                                                                                                                                                                                                         A,Residues: 1-136 <KUR>
A,Cross-references: UNIPROT:099749;
A,Experimental source: strain N315
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VESKSINVEVHLTKK 136
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C,Superfamily: enterotoxin B
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Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
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A; Reference number: A89758; MUD:21311952; PMID:11418146
A; Accession: E8996
A; Accession: E8996
A; Ascession: E8996
A; Residual probleminary
A; Molecule type: DNA
A; Residuales: 1-260 cKUR>
A; Residuales: 1-260 cKUR>
A; Residuales: 1-260 cKUR>
A; Experimental source: strain N315
A; Experimental source: strain N315
A; Genetics:
A; Genetics:
A; Choretics:

                           C,Accession: A3353
K; Bayles, K.W.; Iandolo, J.J.
J; Bacteriol. 171, 4799-4806, 1989
A; Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A; Reference number: A33953; MUID:89359112; PMID:2549000
A; Accession: A33953
A; Accession: A33953
A; Reference rumber: A3953; MUID:89359112; PMID:2549000
A; Reference number: A3953
A; Residual type: DNA
A; Residual type: DNA
A; Residual type: DNA
A; Cross-references: UNIPROY:P20723; GB:M28521; NID:91492109; PIDN:AAB06195.1; PID:975869
C; Superfamily: enterotoxin B
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQ-SLSFD-IETNKKMVTA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LKKM-VFFVLVTFLGLTISQ-EVFAQODPD---PSQLHR-----SSLVKNLQNIYFLYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPVTHENVKSVDQLRSHDLIYN---VSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYY
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36.2%; Pred. No. 8.4e-18;
iive 42; Mismatches 107; Indels 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 340; DB 2; Length 25; Pred. No. 5.9e-18; 47; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||:|| : |::|| | XSDNKTLSTEHLHIDIYLYEK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 YKDNETLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                               25.7%;
ilarity 35.2%;
Conservative 47
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Best Local Similarity 30.2...
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Best Local Similarity
Matches 92; Conserv
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extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus
C;Date: IO-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
R, A.; Milautan-1ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:BA000018; PID:g13701617; PIDN:BAB42910.1; GSPDB:
                                                                                                                                                            69 DKFLAHDLIYNISDKKLKNYDKVKTELLNEGLAKKYKDEVVDVYGSNYYVNCYFSSKDNV 128
                                                                                                                                                                                                                                                                189 KARNFLINKKNLYEFNSSPYETGYIKFIENNGNIFWYDMMPAPGDKFDQSKYLMMYNDNK 248
                                                                                                                                                                                                                                 124 ER----SACIYGGVTNHEGNHLEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDY 177
                                                                                                                                                                                                                                                                                                                                178 KVRKYLTDNKOLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146
A,Accession: G89968
A,Status: preliminary
A,Rolecule type: DNA
A,Residues: 1-258 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GRGVINSRQFLSHDLIFPIEYKSYNEVKTELENTELANNYKDKKVDIFGVPYFYTCIIPK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 DYKARHWLIKEKKLYEPDGSAFESGYIKFIEKNNISFWFDLFPKKELVPFVPYKFLNIYG 239
                                                                                                                                DQLRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                62 HENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCE
                                 MVF-FVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAE-----RSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
36.4%; Score 481; DB 2;
Best Local Similarity 40.7%; Pred. No. 2.3e-28;
Matches 105; Conservative 46; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enterotoxin D precursor - Staphylococcus aureus C; Species: Staphylococcus aureus
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A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|| : :|||:|||
249 TVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                  TLDSNTSQIEVYLTTK 251
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C;Superfamily: enterotoxin B
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus
C;Accession: S66356; A01816
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15.20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness the scension: S66356
A;Molecule type: DNA
A;Reference number: S06356; MUID:88038352; PMID:2823067
A;Tocession: S66356
A;Molecule type: DNA
A;Residues: 1-566 *80H>
A;Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A;Reference number: A01816; MUID:83213327; PMID:6189824
A;Accession: A01816
A;Molecule type: protein
A;Residues: 28-75, IL', 78-176, 'N', 178-266 *SCH>
C;Genetics: enterotoxin B
C;Keywords: enterotoxin B
C;Keywords: enterotoxin B
C;Keywords: enterotoxin B
C;Keywords: enterotoxin C-1 #status experimental *MAT>
F;120-137/Disulfide bonds: #status experimental
E;120-137/Disulfide bonds: #status experimental
                                 A; Reference number: A33866; MUD:89327174; PMID:2473979
A; Reference number: A33866
A; Racession: A33866
A; Racession: A33866
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-266 < COU>
A; Cross-references: GB:MZ8364; NID:g153003; PIDN:AAA26624.1; PID:g153004
C; Genetics:
C; Superfamily: enterotoxin B
F; 1-27/Domain: signal sammar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 ER----SACIYGGVTNHEGNHLEIP--KKIVVKVSIDGIQSLSFDIETNKKMVTAQELDY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKVTGGKTCMYGGITKHEGNHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQLRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 MVF-FVLVTFLGLTISQEVFAQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
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                                                                                                                                                                                                                                                                                                                                                                                                41.5%; Score 549; DB 2; Length 266; 44.1%; Pred. No. 2.3e-33; Live 52; Mismatches 73; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73; Indels
                                                                                                                                                                                                                                                                                                                        F;1-27/Domain: signal sequence #status predicted <SIG>F;28-266/Product: enterotoxin C-2 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
41.5%; Score 548; DB 1;
Best Local Similarity 44.5%; Pred. No. 2.7e-33;
Matches 114; Conservative 51; Mismatches 73;
A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|| ::|||:||||
TVDSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
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enterotoxin C-2 precursor - Staphylococcus aureus
N.Alternate names: enterotoxin C-3 precursor
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: OloNov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60114; B60114; Ā33866
R;Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A;Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A;Reference number: A60114; MUID:89277549; PMID:2543637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene: sequence compari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-266 <HOV>
A;Cross-references: UNIPROT:P23313; GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKXMVTAQELDYK 178
                                   191 TRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 LRSHDLIYNVSG---PNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC--ENAER 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 ----SACIYGGVTNHEGNHLEIP--KKIVVKVSIDGIQSLSFDIETNKKWVTAQELDYKV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 RKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNETL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
Cispecies: 10-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
Cispecies: 13-Mackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Tille: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: seqn
A;Reference number: S11885; MUID:90220508; PMID:2325627
A;Accession: S11885
                                                                                                                    179 VRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEP--EFTQSKYLMIYKDNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 VLVTFLGLTIS-QEVFAQQDPD--PSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.7%; Score 551.5; DB 2;
46.1%; Pred. No. 1.5e-33;
iive 46; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterotoxin C3 - Staphylococcus aureus
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A;Cross-references: UNIPROT:P34071
A;Accession: B60114
A;Molecule type: protein
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VDSKDVKIEVYLTTK 264
                                                                                                                                                                                                                                               LDSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSNTSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || : :|||:||||
|DSKSVKIEVHLTTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 117; Conservative
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                                                                                                                                                                                                                                            237
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A, Molecule type: protein
A, Residues: 28-55, NND', 59-68, NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT', A; Residues: 28-55, NND', 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT', A; Experimental source: strain S-6
R; Huang, I.Y.; Bergdoll, M.S.
B, Huang, I.Y.; Bergdoll, M.S.
A; Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compositing A; Refarence number: A92064; MUID: 71007901; PMID: 5470820
A, Contents: annotation; chymotryptic peptides
R; Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A, Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition, A; Reference number: A92063; MUID: 71007900; PMID: 5470819
                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004
C;Date: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004
C;Datesion: S27360; A92065; $\overline{2}$72240; A01815

B;Jones, C.L.; Khan, S.A.
J; Bacteriol. 166, 29-33, 1986
A;Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A;Reference number: S27360; MUD:86168029; PMID:3957869
A;Reference number: S27360
A;Residues: 1-266 < JON>
A;Residues: 1-266 < JON>
A;Residues: 1-266 < JON>
A;Experimental source: strain S6
A;Experimental source: strain S6
A;Huang, I.Y.; Bergdoll, M.S.
J; Biol. Chem. 245, 3518-3525, 1970
A;Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromid A;Reference number: A92065; MUID:71007902; PMID:5470821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Contents: annotation; tryptic peptides
R; Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.
Biochemistry 4, 1011-1016, 1965
A; Title: Purification of staphylococcal enterotoxin B.
A; Reference number: A90548; MUID: 66035792; PMID: 4953912
A; Contents: annotation; biological source of protein
A; Contents: annotation; biological source of protein
Bur. J. Shakhov, V.Y.; Klinsky, E.Y.; Klosov, M.L.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni
Bur. J. Blochem. 209, 823-828, 1992
A; Title: Identification of functionally active fragments of staphylococcal enterotoxin B
A; Reference number: S27240; MUID: 93049338; PMID: 1425690
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                                                                    180 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRSHDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA----
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A. Molecule type: protein
A. Residues: 28-42;128-148
C. Superfamily: enterotoxin B
C. Keywords: enterotoxin; extracellular protein; toxin
C. Fig. 27/Domán: signal sequence #status predicted <SIG>
F; 28-26/Product: enterotoxin B #status experimental <MAT>
P; 120-140/Disulfide bonds: #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                          enterotoxin B precursor - Staphylococcus aureus
                                                                                                                                                                                        240 TSQIEVYLTTK 250
                                                                                                                                                        241 TSQIEVYLTTK 251
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Best Local Similarity
Matches 123; Conserv
                                   181
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C;Accession: A26152
R;Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exctoxin type A (scarlet fever toxin) is related to Sta
                                                                                                                                                                                                                                                                                        A;Residues: 1-236 <NEL>
A;Cross-references: UNIPROT:Q54696; EMBL:X61573; NID:q47303; PIDN:CAA43771.1; PID:g4730-A;Notes: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DQLRSHDL1YNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 IYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYLTDNKQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THENVKSVDQLLSHDLIXNVSGPNYDKLKTELKNQEMATLFKDKNVDIXGVEYYHLCYLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENAERSACLYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIEQIKN-GNCSRISYTVR 179
                                                                                                                                               the speA
          09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp. NiAlternate names: scarlet fever toxin; SPE type A (speA) (c.species: Streptococcus sp. C.species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DQLLSHDLIYNVSGLNYDKLKTELKORREMSTLFKNKOVDIYGVEYYYHCYLCRNAKRRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 IYGGVTNHEGNHLEIPKNILVKVSIDGIQSLSFDIETSKKMYTAQELDYKVRKHLTDNKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 KKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-JuC;Accession: S18789
R;Nelson, K.; Schlivert, P.M.; Selander, R.K.; Musser, J.M.
B;Nelson, Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18789
A;Accession: S18789
A;Accession: United and sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Keywords: exotoxin E;1-22/Domain: signal sequence (fragment) #status predicted <SIG>F;23-236/Product: exotoxin A (fragment) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; DB 2;
9.1e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 9.1e
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.9%; Score 1109;
88.6%; Pred. No. 9.
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C; Superfamily: enterotoxin B
C; Keywords: exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.4%;
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Matches 209; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Superfamily: enterotoxin
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A, Molecule type: DNA
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A/Status: nucleic acid sequence not shown; translation not shown
A/Accession: S18792
A/Status: nucleic acid sequence not shown; translation not shown
A/Residues: 1-236 < NEO-
A/Status: nucleic acid sequence not shown; translation not shown
A/Residues: 1-236 < NEO-
A/Status: nucleic acid sequence was submitted to the EMBL Data Library, September 1991
A/Accession: S18795
A/Actus: nucleic acid sequence not shown; translation not shown
A/Residues: 1-236 < NEH-
A/Cross-references: EMBL:X61566; NID:947317; PIDN:CA443764.1; PID:947318
A/Accession: S18799
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                                                                                                                      A, Accession: S18788
A, Status: nucleic acid sequence was summittee to the brib data divisity, september 1271
A, Status: nucleic acid sequence not shown; translation not shown
A, Follower: DNA
A, Follower: 1-236 cNEZ>
A, Follower: DNA
A, Esperimental source: EFMBL.X61563; NID:947301; PIDN:CAA43761.1; PID:947302
A, Experimental source: strain MGAS256 isolate California unassigned phage
A, Both Committee acid sequence was submitted to the EMBL Data Library, September 1991
A, Accession: S18790
A, Follower: DNA
A, Follower: DNA
A, Follower: DNA
A, Follower: L-236 cNEY>
A, Coss-references: EMBL.X61564; NID:947305; PIDN:CAA43762.1; PID:947306
A, Experimental source: strain MGAS285 isolate Colorado unassigned phage
A, Experimental source: strain MGAS285 isolate Colorado unassigned phage
A, Experimental source: strain MGAS285 isolate to the EMBL Data Library, September 1991
                            A;Cross-references: EMBL:X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A;Experimental source: strain MGAS251 isolate California unassignd phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
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C,Superfamily: enterotoxin B
C;Reywords: extoxin
C;Reywords: extoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
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93.3%; Score 1234; DB 2;
Best Local Similarity 99.2%; Pred. No. 5.4e-84;
Matches 234; Conservative 0; Mismatches 2;
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A;Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned p A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991 A;Accession: 318797
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 9-244 < NEH>
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A;Residues: 9-244 < NEH>
A;Residues: 9-244 < NEH>
A;Rocession: S18800
A;Accession: S18800
A;Accession: S18800
A;Accession: S18800
A;Accession: S18800
A;Accession: S18800
A;Retus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-228 < NES>
A;Cross-references: EMBL:X61554; NID:947327; PIDN:CAA43752.1; PID:947328
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A;Cross-references: EMBL:X61554; NID:947327; PIDN:CAA43752.1; PID:947328
A;Cross-references: EMBL:X61554; NID:947327; PIDN:CAA43752.1; PID:947328
A;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
A;Gene: speA; speAl
C;Superfamily: enterotoxin B
C;Superfamily: enterotoxin B
C;Superfamily: signal sequence #status predicted <NAT>
F;11-351/Product: exotoxin type A #status predicted <NAT>
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J. Exp. Med. 174, 1271-1274, 1991
A; Title: Characterization and clonal distribution of four alleles of the speA gene encod A; Reference number: S18782; MUID:92044323; PMID:1940804
A; Accession: S18783
A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-236 <NEL>A; Residues: 1-236 <NEL>A; Residues: EMBL: S18782; MID:947289; PIDN:CAA43766.1; PID:947290
A; Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A; Notes: the nucleocide sequence was submitted to the EMBL Data Library, September 1991
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A;Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
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|TSQIEVYLTTK 251
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A; Status: nucleic ad
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exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isol N.Alternate names: scarlet fever toxin
N.Alternate names: scarlet fever toxin
A.Alternate names: scarlet fever toxin
A.Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain isolate United Kingdom; strain MGAS496 isolate Germany
C.Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text change 16-Jul-1999
C.Accession: S18786; S18787; S18789; S18792; S18799; S18799;
R.Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
A.Fitle: Characterization and clonal distribution of four alleles of the speA gene enco. A.Reference number: S18782; MUID:92044323; PMID:1940804
A.Accession: S18786
A.Accession: S18786
A.Accession: S18786
A.Accession: S18786
A.Accession: S18786
A.Accession: S18786
A.Accession: DNA
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A; Residues: 1-236 <NEZ>
A; Cross-references: EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID:947316
A; Cross-references: EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID:947316
A; Cross-references: Errain MGAS491 isolate United Kingdom unassigned phage
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Accession: S18801
A; Accession: S18801
A; Residues: 1-236 <NEY>
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A; Experimental source: strain MGAS624 isolate Germany unassigned phage
A; Mote: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A; Accession: S18798
A; Accession: S18798
A; Accession: DAA
A; Molecule type: D
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A;Residues: 1-236 <NEO>
A;Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324
A;Cross-references: EMBL:X61571; NID:g47325; Esolate Germany unassigned phage
A;Reperimental source: strain MGAS495 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
submitted to the EMBL Data Library, September 1991
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;Reywords: exotoxin
;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
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A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
                                                                                                       shown; translation not shown
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No. 2,3e-84;
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1; Mismatches
                                                           A;Accession: S18794
A;Status: nucleic acid sequence not
          the nucleotide sequence was
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Best Local Similarity 99.2'
Matches 234; Conservative
                                                                                                                                                        A, Molecule type: DNA
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

September 17, 2005, 01:00:14; Search time 18.153 Seconds (without alignments) 1330.382 Million cell updates/sec Run on:

US-10-002-784A-16 1322 1 MENNKKVLKKMVFFVLVTFL......KDNETLDSNTSQIEVYLTTK 251 Perfect score: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25 2 H82885 34 1 XCSAS1 31 2 E89806 96 2 E96935 93 2 G90604 70 2 B46910 24 2 A48910 40 2 137281 67 2 T18466 67 2 C95008 96 2 S09627 35 2 C97252	825 234 231 231 231 231 231 235 235 235 235 235 235 235 235 235 235	hypothetical prote	toxic shock syndro	exotoxin 7 [import	FUSION, methionine	ORF MSV181 hypothe	hypothetical prote	transport protein	desmocollin 1b pre	desmocollin la pre	Dscla precursor -	Dsc1b precursor -	hypothetical prote	immunoglobulin Al	hypothetical prote	prrC protein - Esc	ā
334 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	ਜ ਜਜ	H82885	XCSAS1	H89806	E96935	T28342	G90604	867593	B48910	A48910	137281	137282	T18466	C95008	B8988	S09627	C97252
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8888888877777777 600088888877777777777777777777777777777		109.5	109	108.5	108.5	108	108	105.5	105	105	105	105	104.5	104.5	103.5	103.5	103
109.5 108.5 108.5 108.5 108.5 108.5 108.5 108.7 105.7 104.5 104.5 103.5	1 09 1 1 09 1 09 1 09 1 09 1 09 1 09 1	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

toxin)

J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encomarkerence number: S18782; MVID:92044323; PMID:1940804
A;Accession: S18782
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA 1877430

A;Residues: 9-244 <NEL>
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A;Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288
A;Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigne.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A;Accession: S18789.
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A;Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292
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A;Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294
A;Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned pi
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A;Accession: S18791 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

A; Residues: 9-244 <NRY>
A; Residues: 9-244 <NRY>
A; Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310
A; Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A;Accession: S18796
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DA
A;Molecule 19-244 <NEO>
A;Residues: 9-244 <NEO>
A;Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320

250 VDSKDVKIEVYLTTK 264

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RESULT 15

US-09-751-708A-10

Sequence 10, Application US/09751708A

Publication No. US20030157113A1

GENERAL INFORMATION:

APPLICATW: FERREMAN, David S

ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

CURRENT APPLICATION NUMBER: US/09/751,708A

CURRENT APPLICATION NUMBER: US 60/173,371

PRIOR PILING DATE: 1999-12-28

NUMBER OF SEQ ID NOS: 166

SOFTWARE: PATENTIN VOTSION 3.1

SEQ ID NO 10

LENGTH: 266

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-751-708A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 TRHYLVKNKKLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMMYNDNKM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 VLVTFLGLTIS-QEVFA--QODPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSVDQ
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250 VDSKDVKIEVYLTTK 264
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MEDIUM TYPE: FLOAPY disk

MEDIUM TYPE: FLOAPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/354,948
FILICATION NUMBER: US/10/354,948
CLASSIFICATION: 424
                                                                                                                                                        Indels
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STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                          Query Match 81.4%; Score 1075.5; DB Best Local Similarity 83.7%; Pred. No. 6.7e-85; Matches 210; Conservative 7; Mismatches 33
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REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/580,806
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 255 amino acids
                                                                                   ORGANISM: Streptococcus pyogenes
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
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STATE: Colorado
COUNTRY: U.S.A.
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                                                                                                US-10-937-758A-20
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Sequence 10, Application US/09870759

Patent No. US2002017551A1

GENERAL INFORMATION:

APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REFERENCE: 870759

CURRENT APPLICATION NUMBER: US/09/870,759

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: US 60/208,128

PRIOR PILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 HDLIYNVSGP---NYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENA----- 123
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3 MITNLIRLIIGNSMESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLY
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48.2%; Pred. No. 1.3e-41;
tive 38; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                      Query Match 44.5%; Score 588; DB 15; Best Local Similarity 47.2%; Pred. No. 1.2e-42; Matches 119; Conservative 41; Mismatches 76;
                                                                                          MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-354-948-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus aureus
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SOFTWARE: PatentIn version 3.1
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Matches 123; Conservative
TYPE: amino acid
TOPOLOGY: linear
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FILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE; FILE REFERENCE: 38373-18918
FILE REFERENCE: 38373-18918
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT APPLICATION NUMBER: US/0/378,988
FRIOR APPLICATION NUMBER: US 60/378,988
FRIOR APPLICATION NUMBER: US 60/389,366
FRIOR APPLICATION NUMBER: US 60/406,697
FRIOR PELING DATE: 2002-06-15
FRIOR PELING DATE: 2002-08-29
FRIOR FILING DATE: 2002-08-29
FRIOR FILING DATE: 2002-0-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2002-10-01
FRIOR FILING DATE: 2003-10-02
FRIOR FILING DATE: 2003-10-02
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FRIOR FILING DATE: 2003-10-03
FRIOR FILING DATE: 2003-10-03
FRIOR FILING DATE: 2003-10-03
FRIOR FILING DATE: 2003-01-09
FRIOR FILING DATE: 2003-01-09
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: FILE REFERENCE 650884
CURRENT APPLICATION NUMBER: US/10/937,758A
CURRENT FILING DATE: 2004-09-08
PRIOR APPLICATION NUMBER: 09/650,884
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                                                                                                                                                          ; Sequence 16, Application US/10428817A; Publication No. US20040214783A1; GENERAL INFORMATION:
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Best Local Similarity 83.73
Matches 210; Conservative
                                         240 TSQIEVYLTTK 250
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               241 TSQIEVYLTTK 251
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US-10-428-817A-16
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US-10-937-758A-20
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PUBLICATION NO. US2030157113A1
GENERAL INFORMATION:
APPLICAMY: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REPERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
FIRING PAPLICATION NUMBER: US 60/173,371
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
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Best Local Similarity 83.7%; Pred. No. 6.7e-85;
Matches 210; Conservative 7; Mismatches 33; Indels 1;
                                                                                                                                                                              Length 250;
                                                                                                                                                                                                                     33; Indels
                                                                                                                                                                         DB 9;
                                                                                                                                                                         Score 1075.5; DB Pred. No. 6.7e-85; 7; Mismatches 33
                                                                                    TYPE: PRT

CRGANISM: Streptococcus pyogenes
US-09-870-759-20
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NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
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SEQ ID NO 20
LENGTH: 250
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Matches 210; Conservative
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US-09-751-708A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
98.9%; Score 1308; DB 9;
Best Local Similarity 99.2%; Pred. No. 4.8e-105;
Matches 249; Conservative 0; Mismatches 2;
                                                                  NAME: Skoog, Mark T
REGISTRATION NUMBER: 40,178
REFERENCE/DOCKET NUMBER: 600.346USWO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
APPLICATION NUMBER: 60/032,930
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
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US-10-002-784A-26
Sequence 26, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
                                                                                                                                                   TELEPHONE: 612-332-5300
TELEPAX: 612-332-9081
TELEX: <Unknown-
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
STRANDEDNESS: single
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TSQIEVYLTTK 251
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APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR PILING DATE: 2000-05-30
                                                       ELKNOEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
                                                                         62 ELKNQEMATLFYDKNIDIYGVEYYHLCYLCENAERSACI-GGVTNREGNHLEIPKKIVVK 120
                                                                                                                                                              91 BLKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHEGNHLEIPKKIVVK 150
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2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLRSHDLIYNVSGPNYDKLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR PILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.9%; Score 1136; DB 14; Best Local Similarity 98.2%; Pred. No. 8.9e-90; Matches 217; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion US-10-002-784A-27
                                                                                                                                                                                                                                                                                                                                RESULT 8
US-10-002-784A-27
Sequence 27, Application US/10002784A
Publication No. US20030036644A1
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US-09-870-759-20
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                   APPLICANT: Roggiani, Manuela
APPLICANT: Stochr, Jennifer
APPLICANT: Stochr, Jennifer
APPLICANT: Oblemdorf, Douglas
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
FILE REPERENCE: 600.311USWO
CURRENT APPLICATION NUMBER: US/08/973,331A
CURRENT FILING DATE: 1998-03-12
PRIOR FILING DATE: 1996-06-07
PRIOR FILING DATE: 1996-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PALENTIN Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MENNYKVIKKMYPFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYBGDPV
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Publication No. US20020086813A1
GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OFERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRIN APPLICATION NATA:
APPLICATION NUMBER: US/09/308,830
FILING DATE: 04-Aug-1999
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                     Score 1308; DB 8;
Pred. No. 4.8e-105;
0; Mismatches 2;
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APPLICATION NUMBER: PCT/US97/22228
FILING DATE: 05-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould P.C.
STREET: P.O. Box 2903
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                     98.9%;
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Best Local Similarity
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                                                       KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEFFTQSKYLMIYKDNETLDSN 240
ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
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                                                                                                                                                                                                                             Sequence 163, Application US/10428817A Publication No. US20040214783A1 GENERAL INFORMATION:
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US-08-973-391A-13
Sequence 13, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:
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SEQ ID NO 163
LENGTH: 251
                                                                                                      TSQIEVYLTTK 251
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US-10-428-817A-163
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ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
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Pred. No. 2.9e-106;
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Bacterial Superantigen
Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 29-Jan-2004
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Ur
TELECOMMUNICATION INFORMATION:
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US-10-767-687-16
US-10-767-687-16
Sequence 16, Application US/10767687
Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Sina Bavair
Sina Bavair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 619-2065
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SEQUENCE CHARACTERISTICS
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Best Local Similarity 100.
Matches 251; Conservative
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COUNTRY: USA
                                                                                                                                          TSQIEVYLTTK 251
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                                                                                                                                                                                                                                          DB 8; Length 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Bacterial Superantigen Vaccines FILE REFERENCE: 003/233/SAP CURRENT APPLICATION NUMBER: US/10/002,784A CURRENT FILING DATE: 2001-11-26 PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776 PRIOR FILING DATE: 97-06-25; 98-09-01 NUMBER OF SEQ ID NOS: 40 SOFTWARE: Apple Macintosh Microsoft Word 6.0
                                                                                                                                                                                                                                        100.0%; Score 1322; DB 8;
100.0%; Pred. No. 2.9e-106;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/10002784A Publication No. US20030036644A1 GENERAL INFORMATION:
    TELECOMMUNICATION INFORMATION:
                    TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ulrich, Robert G.
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Best Local Similarity 100.0
Matches 251; Conservative
                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSQIEVYLTTK 251
                                                                                                                   TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
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LENGTH: 251
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CORRESPONDENČE ADDRESS:
ADDRESSER: Charles H. Harris
STREET: US Army MRMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
CITY: FORT DETRICK
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KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
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September 17, 2005, 00:44:58; Search time 77.8484 Seconds (without alignments) 1305.574 Million cell updates/sec
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1. / cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

2. / cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/DS06_PUBCOMB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

3. / cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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6. / cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

7. / cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

8. / cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

9. / cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

9. / cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1812044 seqs, 404927589 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1322
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 16, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 163, App	Sequence 13, Appl	Sequence 13, Appl	Sequence 26, Appl	Sequence 27, Appl	Sequence 20, Appl	Sequence 20, Appl	Segmence 16, Appl
SUMMARIES	QI	8 US-08-882-431-16	US-10-002-784A-16	US-10-767-687-16	US-10-428-817A-163	US-08-973-391A-13	US-09-308-830-13	US-10-002-784A-26	US-10-002-784A-27	US-09-870-759-20	US-09-751-708A-20	US-10-428-817A-16
	DB	8	14	11	16	œ	σ	14	14	6	10	16
	Query Match Length DB	251	251	251	251	251	251	220	468	250	250	250
dip	Query	100.0	100.0	100.0	99.5	98.9	98.9	85.9	85.9	81.4	81.4	81.4
	Score	1322	1322	1322	1315	1308	1308	1136	1136	1075.5	1075.5	1075.5
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7 US-10-937-75	S-10-354-94	-078-09-870-	ūS	16 US-10-428-817A-6	7 US-10-937-	150-94	US-10-17	14 US-10-151-336-8		US-10-002	17 US-10-767-687-6	US-10-002-784	17 US-10-767-687-10	US-10-002-784	17 US-10-767-687-8	B US-08-882-431-10	US-08-882			6 US-10	8 US-08-882-431-6	US-09-870-	9-751-708A	US-10-428-817A		US-10-923-3	16 US-10-428-817A-185	17 US-10-923-324-1	us-	17 US-10-923-324-5	7	.7 US-10-923-324-6	17 US-10-923-324-2	
250			566	. 997											566	-		266	266								239					240	240	
	44.5	43.6	43.6	43.6	43.6	43.6	43.6	43.5	43.4	42.9	42.9	42.6	42.6	42.2	42.2	42.2	41.8	41.8	41.8	41.7	٠	41.5	÷	٠		41.4	41.2	41.1	41.0	40.5	40.5	40.3	40.2	
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12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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US-08-BKZ-411-16

| US-08-BKZ-411-16
| Publication No. US20030009015A1 |
| GENERAL INFORMATION: |
| APPLICANT: Mark A. Olson |
| APPLICANT: SIMB BAVAIN: |
| APPLICANT: SIMB BAVAIN: |
| APPLICANT: SIMB BAVAIN: |
| APPLICANT: SIMB BAVAIN: |
| APPLICANT: SIMB BAVAIN: |
| APPLICANT: SIMB BAVAIN: |
| APPLICANT: SIMB BAVAIN: |
| TITLE OF INVENTION: |
| Vaccines |
| VARMENCES: 16 |
| VORRESPONDENCES: 16 |
| CORRESPONDENCES: 16 |
| APPLICANT OF BATAIN: |
| CONTINE MARYLAND |
| COUNTRY: USA |
| CONTINE READABLE FORM: |
| MEDIUM TYPE: | Floppy disk |
| COMPUTER: Apple Macintosh |
| COMPUTER: Apple Macintosh |
| COMPUTER: Apple Macintosh |
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| CORREST APPLICATION NUMBER: US/08/882,431 |
| FILING DATE: |
| CLASS FFLATION NUMBER: US/08/882,431 |
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NAME: MOTAIL, JOHN
REGISTRATION NUMBER: 26,313
REFERENCE/POCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
US-08-882-431-16
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Roggiani M, Stoehr J,
(MINU ) UNIV MINNESOTA
                                                                          WPI; 1997-099936/09.
                                    Schlievert PM,
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Ohlendorf

Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.

Example 4; Page; 102pp; English.

The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPB-A) mutant, which can be used to produce vaccines to protect animals against wild type SPB-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPB-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPB-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPB-A is cancer. It is thought that mutant SPB-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPB-A sequence given on pages 77-79 

Sequence 251 AA;

ö 1 MENNKKVILKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV 60 0; Gaps Query Match 98.2%; Score 1298; DB 2; Length 251; Best Local Similarity 98.8%; Pred. No. 4.9e-109; Matches 248; Conservative 0; Mismatches 3; Indels (

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ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180 121

TSQIEVYLTTK 251 241

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241 TSQIEVYLTTK 251

Search completed: September 17, 2005, 01:09:41 Job time : 84.0376 secs

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120

180 240 240

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ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR 180
toxin A (SPE-A) mutant, which can be used to produce vaccines to protect toxic shock syndrome (STS-A and to treat cancer and streptococcal toxic shock syndrome (STS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcal; toxin A, SPE-A, non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutraliaing antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THENVKSVDQLLSHHLI YNVSGPNYDKLKTELKNQEMATL-FKDKNVDI YGVEYYHLCYLC
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Pred. No. 3.9e-109;
2; Mismatches 2;
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  Mismatches
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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPB-A) mutant, which can be used to produce vaccines to protect animals against wild type SPB-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPB-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPB-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but
                          KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 240
                                                                                                                                                                                                                                                                                                                                                                                               Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
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KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
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Pred. No. 1.7e-109;
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/label= sig_peptide
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/label= mat_peptide
                                                                                                                                                                                                                                AAW12147 standard; protein; 251 AA.
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98.8%;
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                                                                                   TSQIEVYLITK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Synthetic.
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                                                                                                   Streptococcal; toxin A, SPE-A, non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutraliaing antibody; streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever; hypotension; group A streptococcal infection; myositis; fascitis; liver damage; T cell; lymphoma; ovarian; uterine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant SPB-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.
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                                                               Streptococcus pyogenes Streptococcal toxin A mutant Lys16Asn.
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/label= sig_peptide
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Synthetic.
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Hes 248; Conserv
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Pred. No. 1.1e-109;
1; Mismatches 2;
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98.8%;
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Best Local Similarity 98.8
Matches 248; Conservative
                                                    Roggiani
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Synthetic.
                                                                            WPI; 1997-099936/09.
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                                                 Schlievert PM,
07-JUN-1995;
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The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79
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Pred. No. 1.4e-109;
1; Mismatches 2;
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'label= sig_peptide
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/label= mat_peptide
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98.8%;
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Matches 248; Conservative
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                                                                                                             Misc-difference 187
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and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be electively toxic to T cell lymphoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or treatment of streptococcal infection or toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                              1 MENNIKKVLKKONVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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                                                                                                                                                                                                                                                                                                                             ENAERSACIYGGVTNHEGNHLE1PKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
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                                                                                                                                                      2; Length 251;
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                                                                                                                                                      Score 1308; DB 2;
Pred. No. 6e-110;
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                                                                                                                                                      98.9%;
99.2%;
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Best Local Similarity
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                                                                                                                           Sequence 251 AA;
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This is the amino acid sequence of the Streptococcus pyogenes exotoxin A as change and is nonlethal compared with a protein to wild type SPE-A toxin. The novel mutant Streptococcal SPE-A toxin has at least 1 as change and is nonlethal compared with a protein to wild type SPE-A toxins are nontoxic and can produce antibodies that neutralise wild type SPE-A toxin activity. The toxins can be used in vaccines and therapeutics to generate a protective immune response against streptococcal infection. They can be used to protect against the development of streptococcal toxic shock syndrome (STSS). In addition, streptococcal infection and in methods for stimulating T cell proliferation and in the treatment of cancer. In particular they can be used for treating T cell proliferation and in the treatment of cancer. In particular they can be used for treating T cell lymphomas, and ovarian and uterine cancer
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                                                                                                                                                                                                                                                                                                                                           MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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Pred. No. 6e-110;
0; Mismatches 2; Indels
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/label= sig_peptide
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/label= mat_peptide
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Matches 249; Conservative
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Synthetic.
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Best Local Similarity
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KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN
                                        ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
                                                                                                                                                                                                                                                                                                                                  enterotoxin; cytostatic; gene therapy; cancer; SpE; SpEA.
                                                                                                                                                                                                                                                                                                          Streptococcal pyrogenic exotoxin A (SpEA) sequence.
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                                                                                                                                                                                                                              ADF89839 standard; protein; 251 AA.
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2002US-0406637P.

2002US-0406750P.

2002US-0415310P.

2002US-0415310P.

2003US-0415400P.
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exotoxin;
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15-JUN-2002; 2
28-AUG-2002; 2
29-AUG-2002; 2
01-OCT-2002; 2
                                                                                                                                                                                                                                                                                                                                  Superantigen;
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Length 251;

DB 8;

99.5%; Score 1315;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substantially cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is Streptococcus pyogenes Streptococcal toxin A (S) -A), from which a non-lethal mutant SPE-A, comprising at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer
                                                                                                   61 THENVKSVDQLLSHDLIYNVSGPNYDK1KTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                                                                                                                                                                 1 MENNKKVLKKOWVFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
                                                                                                                                         ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
                                                                                                                                                              ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
                                                                                  THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
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                         1 MENNIKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
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Mismatches
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/label= mat_peptide
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fragment is altered so that binding of the encoded altered toxin DNA fragment is altered so that binding of the encoded altered toxin to ceither the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct, postboring a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin); an altered TSST-1 (toxic shock syndrome toxin) or superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, an antisera isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1 conspicion toxin and an antibody which recognises altered TSST-1 conspicion toxin and an antibody which recognises altered TSST-1 conspicion toxin and an antibody which recognises altered TSST-1 conspicion toxin and an antibody which recognises altered TSST-1 composition for treating or preventing bacterial infection. The present sequence represents the L42A (with reference to the mature protein) composition for treating or preventing bacterial infection. The present sequence represents the L42A (with reference to the mature protein) contained by the indexer using the wild-type sequence expressions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MENNKKVLKKOMVFFVLVTFLGLTISQEVFAQQDPDBSQLHRSSLVKNLQNIYFLYEGDPV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 superantigen toxin DNA fragment, useful for preparing a composition treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
                                                                                     SPEa, streptococcus pyrogenic enterotoxin a, mutant, vaccine, mutein, superantigen toxin; MHC; superantigen-associated bacterial infection; bacterial.
                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Leu substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1316; DB 7;
Pred. No. 1.1e-110;
0; Mismatches 1;
                                         Streptococcus pyrogenic toxin a L42A mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and the information in the specification
                                                                                                                                                                                                                                                                                                             31. .251
/label= Mature_SPEa_L42R
                                                                                                                                                                                                                                                                   1. .30
/label= Signal_peptide
                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 13; Page; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-NOV-2001; 2001US-00002784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00144776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-00882431
27-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-492125/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                           Streptococcus sp. Synthetic.
                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1997;
01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ulrich RG;
                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFFTQSKYLMIYKDNETLDSN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYCVEYYHLCYLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDSN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of vaccines against bacterial superantigen toxin infections. They are also useful in gene therapy. The present sequence is Streptococcus pyogenes pyrogenic exotoxin A (SpeA) protein. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MENNKKVIKKMVFFVLVTFLGLTISQEVFAQODPDPSQLHRSSLVKNLQNIYFLYEGDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                             1. .29
/label= Signal_peptide
30. .251
/note= "S. pyogenes mature SpeA protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1322; DB 7;
Pred. No. 3.3e-111;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            (USME-) US MEDICAL RES INST INFECTIOUS DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 130-131; 141pp; English.
                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 251; Conservative 0
                                                                                                                                                                                                                                                                                                                                    26-NOV-2001; 2001WO-US046540
                                                                                                                                                                                                                                                                                                                                                                                26-NOV-2001; 2001US-00002784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSQIEVYLTTK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TSQIEVYLTTK 251
                                                                   Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-492125/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD56771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 251 AA;
                                                                                                                                                                                                                                            WO2003056015-A1
                       gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ulrich RG;
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Length 251;

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(ULRI/) ULRICH
                  25-JUN-1997;
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                                                                                                                                                                                                                                      Ulrich RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                   and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating superantigen-associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
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                                                                                         invention relates to an isolated and purified superantigen toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1322; DB 6;
100.0%; Pred. No. 3.3e-111;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pyrogenic toxin a L42R mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Mature_SPEa_L42R
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/label= Signal_peptide
    Claim 17; Page 34-35; 50pp; English.
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The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial for infection, a vaccine (comprising an altered superantigen-associated bacterial infection, an area ingland antigenic response resulting in the protection of a mammal against superantigen-associated bacterial infection, an area inglanded from individuals immunised bacterial infection, an antisear isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present superance represents the L42R (with reference to the mature protein)
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                                                                                                                    New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
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100.0%; Pred. No. 3.3e-111;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the protein sequence of Streptococcus pyogenes vaccine SPEa42. The vaccine differs from the native SPEa sequence by substitution of the Leu-42 residue by Arg. This mutation is expected to disrupt contact between the toxin and the HIA-DR receptor, reducing DRI binding. SPEa42 can be expressed as recombinant protein in Escherichia coli as a secreted protein or as a cytoplasmic product. No indicators of toxicity have been detected for the purified recombinant protein, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment superantigen toxin-associated bacterial diseases.
                                                                                            MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
                                                                                                                                   THENVKSVDQLRSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLC
                                                                                                                                                                           ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVR
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                                                                              1 MENNKKVLKKMVFFVLVTFLGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     SPEa; SPEa42; superantigen; antigen; toxin; vaccine;
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0
                                      Length 251;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                 Streptococcal pyrogenic exotoxin A vaccine SPEa42.
                                                3.3e-111;
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0
                                      DB 3;
                                      ;; Score 1322; D
;; Pred. No. 3.3e
0; Mismatches
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                                     ttch 100.0%; sal Similarity 100.0%; 251; Conservative 0
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bacterial infections
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                  Sequence 251 AA;
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vaccine studies demonstrate that SPEa42 is highly antigenic, inducing protective immunity in a mouse animal model. The attenuated superantigen and beased to protect against superantigen toxin infections. Methods of producing and using altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided by the invention. A multivalent rescine consisting of altered superantigen toxins from SEA, SEB, SEC-1, TSST-1 and SPEa is predicted to provide protective immunity against the majority of bacterial superantigen toxins
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N-PSDB; ACA61184.
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September 17, 2005, 00:47:53; Search time 82.0376 Seconds (without alignments) 1183.322 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

uo	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Amino aci	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Streptoco	Amino aci	Amino aci	Streptoco	Streptoco	Staphyloc	Staphyloc
Description	Aay70109	Abb 79508	Abu10088	Abu62331	Aae37683	Abu62460	Adf89839	Aaw12097	Aaw59780	Aaw12154	Aaw12146	Aaw12150	Aaw12147	Aaw12148	Aaw12153	Aaw12151	Aaw12152	Aaw12149	Aaw12145	Aaw59798	Aaw59781	Aab67344	Aar13209	Aar45017	Abb76240
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SUMMARIES	AAY70109	ABB79508	ABU10088	ABU62331	AAE37683	ABU62460	ADF89839	AAW12097	AAW59780	AAW12154	AAW12146	AAW12150	AAW12147	AAW12148	AAW12153	AAW12151	AAW12152	AAW12149	AAW12145	AAW59798	AAW59781	AAB67344	AAR13209	AAR45017	ABB76240
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ABU62334 AAE37687 ABU62335 AAE37684	AAE37689 AAE37688 AAE37691	ABU79074 ADF43300 AAW06737	ABU79069 ABG75015 ADF43290	AAW64647 AAY92319 ABU62454	ADF89825 AAB67341 ABG75016 ADL14247
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22 23 28 29	31		36 37 38	39 41	4 4 4 4 64 64 67

## ALIGNMENTS

Superantigen toxin; SAg; Streptococcal pyrogenic exotoxin A; SPE-A; antibacterial; vaccine; MRC class II receptor; T-cell antigen receptor; cytostatic; antibody; staphylococcal/streptococcal toxin; toxxid; SPEA42; diagnosis; treatment; superantigen-associated bacterial infection. Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections. Streptococcal pyrogenic exotoxin A (SPE-A). AAY70109 standard; protein; 251 AA. (REED-) REED ARMY INST RES WALTER. Bavari S; 98WO-US016766. 98WO-US016766. (first entry) Olson MA, 2000-224177/19. Streptococcus sp. N-PSDB; AAZ51112. WO200009154-A1. 13-AUG-1998; 13-AUG-1998; 05-JUN-2000 24-FEB-2000. Ulrich RG, AAY70109; 

Example 12; Page 94-95; 118pp; English.

The present amino acid sequence is the Streptococcal pyrogenic exotoxin A (SPE-A), a bacterial superantigen toxin (SAg), used for the formulation of SPE-A vaccine SPEA42. The coding region of this SAg toxin is altered by site directed mutagenesis, introducing L42R mutation, that results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SPE-A has antibacterial and cytostatic activity. This sequence is useful for the production of SPE-A vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxonical against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated